

CAA04703.1	AJ001370	Olea europaea cytochrome b5. cytob5-2.
AAA32990.1	M87514	Brassica oleracea cytochrome b-5. cytochrome b-5.
CAA50575.1	X71441	Nicotiana tabacum cytochrome b5.
CAA53366.1	X75670	Oryza sativa cytochrome b5.
CAA04702.1	AJ001369	Olea europaea cytochrome b5. cytob5-1.
AAA62621.1	L22209	Cuscuta reflexa associated with cytokinin-induced haustoria formation in Cuscuta reflexa. cytochrome b5.
AAC49701.1	U79011	Borago officinalis haem-binding protein. cytochrome b5.
CAA56318.1	X80008	Nicotiana tabacum cytochrome b5.
CAA48240.1	X68140	Nicotiana tabacum cytochrome b5.
AAD10774.1	AF098510	Petunia x hybrida involved in anthocyanin biosynthesis. cytochrome b5 DIF-F. diffF. required for full activity of flavonoid 3',5' hydroxylase.
AAF60299.1	AF233640	Petunia x hybrida involved in anthocyanin biosynthesis. cytochrome b5 DIF-F. diffF.
CAA11033.1	AJ222981	Physcomitrella patens delta6-acyl-lipid desaturase. des6. des6 represents a fusion between a C-terminal desaturase with a cytochrome b5-related part and a N-terminal extension.
SEQ ID NO: 392		
AAK28303.1	AF346431	Nicotiana tabacum phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.
AAB36653.1	U32644	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS5a.
BAB17061.1	AP002523	Oryza sativa putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).
AAB36652.1	U32643	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.
BAB17059.1	AP002523	Oryza sativa putative glucosyl transferase. P0013F10.5.
BAB17060.1	AP002523	Oryza sativa putative glucosyl transferase. P0013F10.6.
CAA59450.1	X85138	Lycopersicon esculentum tw1. homologous to glucosyltransferases.

CAB56231.1 Y18871 *Dorotheanthus bellidiformis*  
betanidin-5-O-glucosyltransferase.

BAA83484.1 AB031274 *Scutellaria baicalensis*  
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

AAB48444.1 U82367 *Solanum tuberosum*  
UDP-glucose glucosyltransferase.

BAA36410.1 AB012114 *Vigna mungo*  
UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

CAA54610.1 X77460 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT4.

CAB88666.1 AJ400861 *Cicer arietinum*  
flavonoid glucosyltransferase. putative UDP-glycose.

AAK16180.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.21.

AAD51778.1 AF116858 *Phaseolus vulgaris*  
utilizes UDPX as the sugar donor and catalyzes the formation of O-xylosylzeatin from zeatin.  
zeatin O-xylosyltransferase. ZOX1.

AAD04166.1 AF101972 *Phaseolus lunatus*  
catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

BAA89009.1 AB027455 *Petunia x hybrida*  
anthocyanin 5-O-glucosyltransferase. PH1.

CAC09351.1 AL442007 *Oryza sativa*  
putative glucosyltransferase. H0212B02.7.

AAB62270.1 AF006081 *Solanum berthaultii*  
UDPG glucosyltransferase. PLGT.

AAK16172.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.14.

AAF61647.1 AF190634 *Nicotiana tabacum*  
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

CAA54612.1 X77462 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT5.

AAK16181.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.16.

AAK16178.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.5.

BAA36412.1 AB012116 *Vigna mungo*  
UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

AAK16175.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.15.

AAF98390.1 AF287143 *Brassica napus*  
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

BAA36423.1 AB013598 *Verbena x hybrida*  
UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

AAF17077.1 AF199453 *Sorghum bicolor*  
UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.

BAA93039.1 AB033758 *Citrus unshiu*  
limonoid UDP-glucosyltransferase. LGTase.

BAB17176.1 AP002843 *Oryza sativa*  
putative UTP-glucose glucosyltransferase. P0407B12.13.

BAB17182.1 AP002843 *Oryza sativa*  
putative UTP-glucose glucosyltransferase. P0407B12.19.

BAA89008.1 AB027454 *Petunia x hybrida*  
anthocyanidin 3-O-glucosyltransferase. PGT8.

CAA54558.1 X77369 *Solanum melongena*  
glycosyl transferase. GT.

CAA54611.1 X77461 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT2.

CAA54609.1 X77459 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT1.

BAA12737.1 D85186 *Gentiana triflora*  
UDP-glucose:flavonoid-3-glucosyltransferase.

AAD21086.1 AF127218 *Forsythia x intermedia*  
adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.

AAG25643.1 AF303396 *Phaseolus vulgaris*  
UDP-glucosyltransferase HRA25. putative; defense associated.

BAA36411.1 AB012115 *Vigna mungo*  
UDP-glucose:flavonoid glycosyltransferase. UFGlyT.

BAA19155.1 AB000623 *Nicotiana tabacum*  
glucosyl transferase. JIGT.

AAD55985.1 AF165148 *Petunia x hybrida*  
catalyzes the penultimate step of flavonol glucosylgalactoside biosynthesis from UDP-galactose and flavonol aglycones in petunia pollen. UDP-galactose:flavonol 3-O-galactosyltransferase. F3galtase.

CAA54613.1 X77463 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT6.

BAA36421.1 AB013596 *Perilla frutescens*  
UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.

BAA19659.1 AB002818 *Perilla frutescens*  
flavonoid 3-O-glucosyltransferase. UDP glucose.

AAB81683.1 AF000372 *Vitis vinifera*  
UDP glucose:flavonoid 3-O-glucosyltransferase.

BAB41025.1 AB047098 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

BAB41023.1 AB047096 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.

SEQ ID NO: 393

CAB56756.1 AJ011589 *Pisum sativum*  
5,10-methylenetetrahydrofolate dehydrogenase: 5,10-methenyltetrahydrofolate cyclohydrolase. bifunctional enzyme.

AAD01907.1 AF030516 *Pisum sativum*  
5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase. bifunctional protein; 31.3 kDa protein.

AAG48834.1 AC084218 *Oryza sativa*  
similar to *Pisum sativum* methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) (AF030516).

SEQ ID NO: 406

AAD46491.1 AF135014 *Zea mays*  
dihydrolipoamide S-acetyltransferase. pyruvate dehydrogenase complex E2 subunit.

BAA90623.1 AP001129 *Oryza sativa*  
ESTs AU033004(S0924),C74754(E50863) correspond to a region of the predicted gene.; Similar to Rat mRNA for dihydrolipoamide acetyltransferase. (D10655).

BAA77024.1 AB026124 *Lithospermum erythrorhizon*  
dihydrolipoamide acetyltransferase.

SEQ ID NO: 407

AAF69017.1 AF261654 *Dianthus caryophyllus*  
ethylene-insensitive 3-like protein 1. EIL1. EIN3-like protein.

CAC09582.1 AJ298994 *Fagus sylvatica*  
gibberellic acid (GA3)-induced. ethylene insensitive (EIN3/EIL)-like transcription regulator. einl1.

AAG00419.1 AF247568 *Nicotiana tabacum*  
EIN3. component in ethylene signal transduction pathway.

SEQ ID NO: 408

AAC15870.1 AF002016 *Cucurbita sp.*  
acyl CoA oxidase homolog.

AAF14635.1 AF202987 *Petroselinum crispum*  
acyl-CoA oxidase. ACO. peroxisomal acyl-CoA oxidase.

AAB67883.1 U66299 *Phalaenopsis sp. 'True Lady'*  
acyl-CoA oxidase homolog.

AAC32108.1 AF051203 *Picea mariana*  
acyl-CoA oxidase homolog. Sb06. similar to *Phalaenopsis* sp. acyl-CoA oxidase homolog  
encoded by GenBank Accession Number U66299.

CAA04688.1 AJ001341 *Hordeum vulgare*  
putative acyl-CoA oxidase.

BAB08201.1 AP002539 *Oryza sativa*  
ESTs AU056822(S20908),C26441(C12328), C28477(C61243) correspond to a region of the  
predicted gene. Similar to *Arabidopsis thaliana* putative acyl-coA dehydrogenase (AF049236).

BAA96762.1 AP002521 *Oryza sativa*  
ESTs AU056822(S20908),C26441(C12328), C28477(C61243) correspond to a region of the  
predicted gene. Similar to *Arabidopsis thaliana* putative acyl-coA dehydrogenase (AF049236).

CAB55555.1 AJ010946 *Pisum sativum*  
auxin binding protein (ABP44). abp44/ivdh. has both auxin binding capability and enzymatic  
activity; isovaleryl-CoA Dehydrogenase.

CAB55554.1 AJ010945 *Pisum sativum*  
auxin binding protein (ABP44). abp44/ivdh. has both auxin binding capability and enzymatic  
activity; Isovaleryl-CoA Dehydrogenase.

CAC08233.1 AJ278987 *Solanum tuberosum*  
leucine catabolism. isovaleryl-CoA dehydrogenase. ivd1.

CAC08234.1 AJ278988 *Solanum tuberosum*  
leucine catabolism. isovaleryl-CoA dehydrogenase. ivd2.

AAF02449.1 AF127432 *Picea abies*  
acyl-CoA oxidase homolog. Sb06.

AAF02451.1 AF127434 *Picea abies*  
acyl-CoA oxidase homolog. Sb06.

AAF02450.1 AF127433 *Picea abies*  
acyl-CoA oxidase homolog. Sb06.

AAC32152.1 AF051733 *Picea mariana*  
acyl-CoA oxidase homolog. Sb06.

AAC32153.1 AF051734 *Picea mariana*  
acyl-CoA oxidase homolog. Sb06.

CAA58874.1 X84055 *Hordeum vulgare*  
mammalian acyl CoA oxidase homologous. cdr29. putative.

SEQ ID NO: 409

CAB64356.1 AJ251511 *Populus tremula x Populus tremuloides*  
mitochondrial oxidase. alternative oxidase. aox1.

AAC60576.1 S71335 *Mitochondrion Nicotiana tabacum*  
alternative oxidase. Aox1. This sequence comes from Fig. 1; AOX.

CAA56163.1 X79768 *Nicotiana tabacum*  
alternative oxidase. aox.

CAA48653.1 X68702 *Glycine max*  
alternative oxidase. aox1. putative.

AAC35354.1 AF083880 *Glycine max*  
alternative oxidase precursor. Aox1. AOX1; terminal oxidase of mitochondrial electron transport chain.

BAB21500.1 AB055060 *Catharanthus roseus*  
alternative oxidase.

BAA23803.1 AB009395 *Catharanthus roseus*  
alternative oxidase.

BAA86963.1 AB007452 *Oryza sativa*  
alternative oxidase. Aox1(Ao1-1).

BAA28773.1 AB004864 *Oryza sativa*  
alternative oxidase. AOX1a.

BAA28772.1 AB004813 *Oryza sativa*  
alternative oxidase. AOX1a.

CAA78823.1 Z15117 *Sauromatum guttatum*  
salicylic acid-inducible alternative oxidase. aox1.

AAA34048.1 M60330 *Sauromatum guttatum*  
alternative oxidase protein. aox1.

AAD51707.1 AF174004 *Triticum aestivum*  
alternative oxidase.

CAA55892.1 X79329 *Mangifera indica*  
alternative oxidase. AOMI 1.

CAB72441.1 AJ271889 *Populus tremula x Populus tremuloides*  
mitochondrial oxidase. alternative oxidase. aox1b.

AAB97285.1 U87906 *Glycine max*  
alternative oxidase. Aox2.

BAA28771.1 AB004813 *Oryza sativa*  
alternative oxidase. AOX1b.

BAA28774.1 AB004865 *Oryza sativa*  
alternative oxidase. AOX1b.

AAB97286.1 U87907 *Glycine max*  
alternative oxidase. Aox3.

AAB97839.1 AF040566 *Zea mays*  
alternative oxidase. Aox.

AAG33634.1 AF314255 *Chlamydomonas reinhardtii*  
alternative oxidase 2. AOX2.

AAG02081.1 AF285187 *Chlamydomonas reinhardtii*  
alternative oxidase. AOX2.

AAG33633.1 AF314254 *Chlamydomonas reinhardtii*  
alternative oxidase 1. AOX1.

AAC05743.2 AF047832 *Chlamydomonas reinhardtii*  
alternative oxidase. AOX1.

BAA23725.1 AB009087 *Chlamydomonas sp. W80*  
alternative oxidase.

AAC34192.1	S81466	Glycine max alternative oxidase Aox1 precursor. Aox1. This sequence comes from Fig. 1.
AAG18450.1	AF302932	Lycopersicon esculentum plastid quinol oxidase.
AAG18449.1	AF302931	Lycopersicon esculentum plastid quinol oxidase.
AAG02287.1	AF177980	Lycopersicon esculentum plastid terminal oxidase. PTOX.
AAG02286.1	AF177979	Lycopersicon esculentum plastid terminal oxidase. PTOX.
AAG02288.1	AF177981	Capsicum annuum plastid terminal oxidase. PTOX.
AAB36072.1	S81470	Glycine max Aox2. Aox2. alternative oxidase 2; This sequence comes from Fig. 1.
AAC35554.2	AF085174	Oryza sativa oxidase. IM1.
AAG00450.1	AF274001	Triticum aestivum oxidase. IM1.
SEQ ID NO: 410		
CAA69600.1	Y08292	Nicotiana plumbaginifolia NADH glutamate dehydrogenase. GDH A.
CAB94836.1	AJ277949	Nicotiana plumbaginifolia NADH glutamate dehydrogenase. gdhA.
CAC18730.1	AJ303070	Vitis vinifera NADH glutamate dehydrogenase. gdhA.
CAA60507.1	X86924	Vitis vinifera glutamate dehydrogenase. GDH.
BAA08445.1	D49475	Zea mays glutamate dehydrogenase.
AAB51596.1	U93561	Zea mays glutamate dehydrogenase. GDH1. wild type.
AAB51595.1	U93560	Zea mays glutamate dehydrogenase mutant. GDH1. mutant allele.
CAB94837.1	AJ277950	Nicotiana plumbaginifolia NADH-glutamate dehydrogenase. gdhB.
CAA09478.1	AJ011096	Asparagus officinalis glutamate dehydrogenase. gdhb.
CAA69601.2	Y08293	Nicotiana plumbaginifolia NADH glutamate dehydrogenase. GDH B.
AAB39508.1	U48695	Lycopersicon esculentum glutamate dehydrogenase. legdh1.

CAA09456.1 AJ011006 *Asparagus officinalis*  
NADH glutamate dehydrogenase. gdhA.

CAA41635.1 X58831 *Chlorella sorokiniana*  
glutamate dehydrogenase (NADP+). gdhANC. There are other coding exons before the first exon given for this gene.

CAA41636.1 X58832 *Chlorella sorokiniana*  
glutamate dehydrogenase (NADP+). gdhANC.

SEQ ID NO: 412

CAA65456.2 X96681 *Oryza sativa*  
transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.

AAK00416.1 AC069324 *Oryza sativa*  
Putative DNA-binding protein. OSJNBA0071K19.2.

BAA05622.1 D26573 *Daucus carota*  
transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.

BAA05625.1 D26576 *Daucus carota*  
transcriptiional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.

BAA21017.1 D26578 *Daucus carota*  
transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.

BAA05624.1 D26575 *Daucus carota*  
transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.

BAA05623.1 D26574 *Daucus carota*  
tranciptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.

SEQ ID NO: 414

BAA95814.1 AP002069 *Oryza sativa*  
ESTs AU082579(S2069),D40238(S2069) correspond to a region of the predicted gene.  
Similar to *Arabidopsis thaliana* vesicle-associated membrane protein 7C; synaptobrevin 7C.  
(AF025332).

SEQ ID NO: 415

CAA45025.1 X63431 *Rauvolfia mannii*  
strictosidine synthase. str1.

CAA68725.1 Y00756 *Rauvolfia serpentina*  
strictosidine synthase.

CAA44208.1 X62334 *Rauvolfia serpentina*  
strictosidine synthase. str1.

CAA37671.1 X53602 *Catharanthus roseus*  
strictosidine synthase precursor.

CAA71255.1 Y10182 *Catharanthus roseus*  
strictosidine synthase. str1.

CAA43936.1 X61932 *Catharanthus roseus*

strictosidine synthase. sss.

AAF75751.1 AF261141 *Lycopersicon esculentum*  
putative strictosidine synthase.

CAB53484.1 AJ245900 *Oryza sativa*

CAA303711.1 protein. q3037.11. Similar to strictosidine synthase 3 precursor.

SEQ ID NO: 418

AAG22607.1 AF258810 *Lycopersicon esculentum*  
aldehyde oxidase. AO3. molybdenum cofactor-binding enzyme.

AAG22606.1 AF258809 *Lycopersicon esculentum*  
aldehyde oxidase. AO2. molybdenum cofactor-binding enzyme.

AAG22605.1 AF258808 *Lycopersicon esculentum*  
aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

BAA23227.1 D88452 *Zea mays*  
aldehyde oxidase-2. zmAO-2. putative.

BAA23226.1 D88451 *Zea mays*  
aldehyde oxidase. zmAO-1.

AAB41742.1 U82559 *Lycopersicon esculentum*  
aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

AAG22608.1 AF259793 *Lycopersicon esculentum*  
aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

AAB41741.1 U82558 *Lycopersicon esculentum*  
aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

SEQ ID NO: 421

BAA13635.1 D88530 *Spinacia oleracea*  
serine acetyltransferase.

BAA13634.1 D88529 *Spinacia oleracea*  
serine acetyltransferase.

BAA93050.1 AB040502 *Allium tuberosum*  
serine acetyltransferase. ASAT5.

BAA08479.1 D49535 *Citrullus lanatus*  
serine acetyltransferase.

BAA12843.1 D85624 *Citrullus lanatus*  
serine acetyltransferase. Sat.

BAA21827.1 AB006530 *Citrullus lanatus*  
serine acetyltransferase. Sat.

AAF19000.1 AF212156 *Allium cepa*  
serine acetyltransferase.

SEQ ID NO: 422

BAA05079.1	D26086	Petunia x hybrida zinc-finger protein.
CAB77055.1	Y18788	Medicago sativa putative TFIIIA (or kruppel)-like zinc finger protein.
AAD26942.1	AF119050	Datisca glomerata zinc-finger protein 1. zfp1. DgZFP1.
AAB39638.1	U68763	Glycine max putative transcription factor. SCOF-1. scoff-1. zinc-finger protein.
AAC06243.1	AF053077	Nicotiana tabacum transcription factor. osmotic stress-induced zinc-finger protein. zfp.
BAA05077.1	D26084	Petunia x hybrida zinc-finger DNA binding protein.
BAA05076.1	D26083	Petunia x hybrida zinc-finger DNA binding protein.
BAA05078.1	D26085	Petunia x hybrida zinc-finger DNA binding protein.
AAK01713.1	AF332876	Oryza sativa zinc finger transcription factor ZF1.
AAB53260.1	U76554	Brassica rapa transcription factor. zinc-finger protein-1. BR42.
AAB53261.1	U76555	Brassica rapa zinc-finger protein BcZFP1. BcZFP1(3-2z).
BAA96070.1	AB035132	Petunia x hybrida C2H2 zinc-finger protein ZPT2-10. PEThy;ZPT2-10.
BAA21919.1	AB006597	Petunia x hybrida ZPT2-10. C2H2 zinc finger protein, 2 finger.
BAA96071.1	AB035133	Petunia x hybrida C2H2 zinc-finger protein ZPT3-3. ZPT3-3.
BAA21927.1	AB006605	Petunia x hybrida ZPT3-3. C2H2 zinc finger protein, 3 finger.
BAA19112.1	AB000453	Petunia x hybrida PEThy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.
BAA21928.1	AB006606	Petunia x hybrida ZPT4-4. C2H2 zinc finger protein, 4 finger.
BAA21922.1	AB006600	Petunia x hybrida ZPT2-13. C2H2 zinc finger protein, 2finger.
BAA19114.1	AB000455	Petunia x hybrida PEThy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
BAA21920.1	AB006598	Petunia x hybrida ZPT2-11. C2H2 zinc finger protein, 2finger.
BAA21921.1	AB006599	Petunia x hybrida ZPT2-12. C2H2 zinc finger protein, 2 finger.

BAA19110.1 AB000451 Petunia x hybrida  
 PEThy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21926.1 AB006604 Petunia x hybrida  
 ZPT2-9. C2H2 zinc finger protein, 2 finger.

BAA21925.1 AB006603 Petunia x hybrida  
 ZPT2-8. C2H2 zinc finger protein, 2 finger.

CAA60828.1 X87374 Pisum sativum  
 putative zinc finger protein.

BAA19111.1 AB000452 Petunia x hybrida  
 PEThy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21923.1 AB006601 Petunia x hybrida  
 ZPT2-14. C2H2 zinc finger protein, 2 finger.

BAA21924.1 AB006602 Petunia x hybrida  
 ZPT2-7. C2H2 zinc finger protein, 2 finger.

BAA19113.1 AB000454 Petunia x hybrida  
 PEThy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.

BAA19926.1 AB000456 Petunia x hybrida  
 PEThy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

SEQ ID NO: 423

AAC49815.1 U87257 Daucus carota  
 4-hydroxyphenylpyruvate dioxygenase.

CAA04245.1 AJ000693 Hordeum vulgare  
 4-hydroxyphenylpyruvate dioxygenase.

SEQ ID NO: 424

AAC72193.1 AF069909 Zea mays  
 pyruvate dehydrogenase E1 beta subunit isoform 2.

AAC72192.1 AF069908 Zea mays  
 pyruvate dehydrogenase E1 beta subunit isoform 1.

AAC72194.1 AF069910 Zea mays  
 pyruvate dehydrogenase E1 beta subunit isoform 3.

AAB01223.1 U56697 Pisum sativum  
 pyruvate dehydrogenase E1beta.

AAC32149.1 AF051249 Picea mariana  
 pyruvate dehydrogenase E1 beta subunit. Sb68.

AAF43837.1 AF166114 Chloroplast Mesostigma viride  
 beta subunit of pyruvate dehydrogenase E1 component. odpB.

AAD22077.1 AF124755 Pinus banksiana  
 pyruvate dehydrogenase E1 beta subunit. Sb68.

CAA75778.1 Y15782 Capsicum annuum  
 transketolase 2.

AAB88295.1 AF024512 Oryza sativa  
 CLA1 transketolase-like protein. CLA1. similar to Arabidopsis CLA1 product; required for chloroplast development.

## SEQ ID NO: 426

AAB53764.1 U96713 *Brassica rapa*  
aminoalcoholphosphotransferase. AAPT1.

AAD56040.1 AF183933 *Brassica rapa*  
aminoalcoholphosphotransferase. AAPT3.

AAC79507.1 U96439 *Pimpinella brachycarpa*  
aminoalcoholphosphotransferase. AAPTase.

AAA67719.1 U12735 *Glycine max*  
CDP-choline:diacylglycerol cholinephosphotransferase activity and possibly CDP-  
ethanolamine: diacylglycerol ethanolaminephosphotransferase activity.  
aminoalcoholphosphotransferase. AAPT1.

## SEQ ID NO: 427

CAA56313.1 X79992 *Avena sativa*  
putative pp70 ribosomal protein S6 kinase. Aspk11.

CAB89082.1 AJ277534 *Asparagus officinalis*  
S6 ribosomal protein kinase. pk1. putative.

AAK18843.1 AC082645 *Oryza sativa*  
putative protein kinase. OSJNBb0033N16.3.

AAC05084.1 AF033097 *Avena sativa*  
NPH1-2. NPH1-2. putative serine/threonine protein kinase.

AAC05083.1 AF033096 *Avena sativa*  
NPH1-1. NPH1-1. putative serine/threonine protein kinase.

AAK13156.1 AC078829 *Oryza sativa*  
putative protein kinase. OSJNBa0026O12.14.

AAB88817.1 AF033263 *Zea mays*  
signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative  
serine/threonine kinase; similar to oat NPH1 proteins.

CAB82852.1 Z30329 *Mesembryanthemum crystallinum*  
protein kinase MK6.

BAB18104.1 AB042714 *Chlamydomonas reinhardtii*  
cyclic nucleotide dependent protein kinase. CL-PK1.

BAB18105.1 AB042715 *Chlamydomonas reinhardtii*  
cyclic nucleotide dependent protein kinase II. CL-PK2.

BAA83689.1 AB011968 *Oryza sativa*  
OsPK7. OsPK7. protein kinase.

AAD31900.1 AF145482 *Mesembryanthemum crystallinum*  
putative serine/threonine protein kinase.

BAA92970.1 AP001551 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F28A21 ; putative protein kinase.  
(AL035526).

BAA92972.1 AP001551 *Oryza sativa*  
ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene.  
Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F6I18 ; putative protein kinase.  
(AL022198).

BAA83688.1 AB011967 *Oryza sativa*  
OsPK4. OsPK4. protein kinase.

AAF22219.1 AF141378 *Zea mays*  
protein kinase PK4. ZmPK4.

CAA73067.1 Y12464 *Sorghum bicolor*  
serine/threonine kinase. SNFL1.

BAA96628.1 AP002482 *Oryza sativa*  
ESTs D41739(S4522),AU055999(S20214), AU057588(S21592 correspond to a region of the  
predicted gene. Similar to *Sorghum bicolor* serine/threonine kinase (Y12465).

CAA89202.1 Z49233 *Chlamydomonas eugametos*  
calcium-stimulated protein kinase.

CAA73068.1 Y12465 *Sorghum bicolor*  
serine/threonine kinase. SNFL2.

BAA34675.1 AB011670 *Triticum aestivum*  
wpk4 protein kinase. wpk4.

CAA74646.1 Y14274 *Sorghum bicolor*  
putative serine/threonine protein kinase. SNFL3.

AAF06970.1 AF162662 *Kalanchoe fedtschenkoi*  
phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.

AAF06969.1 AF162661 *Kalanchoe fedtschenkoi*  
phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.

CAA39936.1 X56599 *Daucus carota*  
calcium- dependent protein kinase. DcPK431.

BAA99439.1 AP002743 *Oryza sativa*  
putative protein kinase. P0710E05.26. contains ESTs C22394(C30013),C22393(C30013).

BAA90814.1 AP001168 *Oryza sativa*  
ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.;  
Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).

BAB12687.1 AP002746 *Oryza sativa*  
putative protein kinase. P0671B1.2. contains ESTs C22394(C30013),C22393(C30013).

AAB62693.1 AF004947 *Oryza sativa*  
protein kinase.

CAA71142.1 Y10036 *Cucumis sativus*  
SNF1-related protein kinase.

BAA05649.1 D26602 *Nicotiana tabacum*  
protein kinase.

AAC25423.1 AF072908 *Nicotiana tabacum*  
calcium-dependent protein kinase. CDPK1.

AAF19403.1 AF203481 *Lycopersicon esculentum*  
phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.

AAF21062.1 AF216527 *Dunaliella tertiolecta*  
calcium-dependent protein kinase. CPK1; CDPK.

AAF19402.1 AF203480 *Lycopersicon esculentum*  
phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.

CAA65244.1 X95997 *Solanum tuberosum*  
SNF1-related protein kinase. PKIN1.

CAA57898.1 X82548 *Hordeum vulgare*  
SNF1-related protein kinase. BKIN2.

BAA13608.1 D88399 *Oryza sativa*  
serine-threonine kinase. endosperm kinase. REK.

CAA08995.1 AJ010091 *Brassica napus*  
MAP3K alpha 1 protein kinase. MAP3K alpha 1.

AAF19401.1 AF203479 *Glycine max*  
phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.

BAA05648.1 D26601 *Nicotiana tabacum*  
protein kinase.

AAC69450.1 AF032465 *Nicotiana tabacum*  
putative serine/threonine protein kinase. WAPK.

AAD23582.1 AF128443 *Glycine max*  
probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.

AAD00239.1 U73938 *Nicotiana tabacum*  
protein kinase. PK11-C1. PK11-C1. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.

AAG60195.1 AC084763 *Oryza sativa*  
protein kinase REK. OSJNBa0027P10.6.

SEQ ID NO: 428

CAC17753.1 AJ294543 *Dendrobium 'Sonia'*  
metabolic enzyme of cytokinins. cytokinin oxidase. cko1.

CAC17752.1 AJ294542 *Dendrobium 'Sonia'*  
metabolic enzyme of cytokinins. cytokinin oxidase. cko1.

CAA77151.1 Y18377 *Zea mays*  
cytokinin oxidase. cko.

AAC27500.1 AF044603 *Zea mays*  
cytokinin oxidase. ckx1.

BAB07927.1 AP002836 *Oryza sativa*  
putative cytokinin oxidase. P0512G09.9.

BAB03420.1 AP002816 *Oryza sativa*  
Similar to *Zea mays* mRNA for cytokinin oxidase. (Y18377).

SEQ ID NO: 429

BAA21922.1 AB006600 *Petunia x hybrida*

ZPT2-13. C2H2 zinc finger protein, 2finger.

BAA21923.1 AB006601 *Petunia x hybrida*

ZPT2-14. C2H2 zinc finger protein, 2 finger.

BAA21921.1 AB006599 *Petunia x hybrida*

ZPT2-12. C2H2 zinc finger protein, 2 finger.

BAA19110.1 AB000451 *Petunia x hybrida*

PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21925.1 AB006603 *Petunia x hybrida*

ZPT2-8. C2H2 zinc finger protein, 2 finger.

BAA21926.1 AB006604 *Petunia x hybrida*

ZPT2-9. C2H2 zinc finger protein, 2 finger.

BAA21924.1 AB006602 *Petunia x hybrida*

ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA19111.1 AB000452 *Petunia x hybrida*

PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA05077.1 D26084 *Petunia x hybrida*

zinc-finger DNA binding protein.

AAD26942.1 AF119050 *Datiscà glomerata*

zinc-finger protein 1. zfp1. DgZFP1.

BAA05076.1 D26083 *Petunia x hybrida*

zinc-finger DNA binding protein.

CAB77055.1 Y18788 *Medicago sativa*

putative TFIIIA (or kruppel)-like zinc finger protein.

AAC06243.1 AF053077 *Nicotiana tabacum*

transcription factor. osmotic stress-induced zinc-finger protein. zfp.

BAA21927.1 AB006605 *Petunia x hybrida*

ZPT3-3. C2H2 zinc finger protein, 3 finger.

BAA96071.1 AB035133 *Petunia x hybrida*

C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

BAA21920.1 AB006598 *Petunia x hybrida*

ZPT2-11. C2H2 zinc finger protein, 2finger.

AAB53261.1 U76555 *Brassica rapa*

zinc-finger protein BcZFP1. BcZFP1(3-2z).

AAB53260.1 U76554 *Brassica rapa*

transcription factor. zinc-finger protein-1. BR42.

CAA60828.1 X87374 *Pisum sativum*

putative zinc finger protein.

AAB39638.1 U68763 *Glycine max*  
 putative transcription factor. SCOF-1. scof-1. zinc-finger protein.  
 AAK01713.1 AF332876 *Oryza sativa*  
 zinc finger transcription factor ZF1.  
 BAA05079.1 D26086 *Petunia x hybrida*  
 zinc-finger protein.  
 BAA96070.1 AB035132 *Petunia x hybrida*  
 C2H2 zinc-finger protein ZPT2-10. PEThy;ZPT2-10.  
 BAA21919.1 AB006597 *Petunia x hybrida*  
 ZPT2-10. C2H2 zinc finger protein, 2 finger.  
 BAA05078.1 D26085 *Petunia x hybrida*  
 zinc-finger DNA binding protein.  
 BAA19112.1 AB000453 *Petunia x hybrida*  
 PEThy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.  
 BAA19114.1 AB000455 *Petunia x hybrida*  
 PEThy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.  
 BAA21928.1 AB006606 *Petunia x hybrida*  
 ZPT4-4. C2H2 zinc finger protein, 4 finger.  
 BAA19926.1 AB000456 *Petunia x hybrida*  
 PEThy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

SEQ ID NO: 432

AAC05084.1 AF033097 *Avena sativa*  
 NPH1-2. NPH1-2. putative serine/threonine protein kinase.  
 AAC05083.1 AF033096 *Avena sativa*  
 NPH1-1. NPH1-1. putative serine/threonine protein kinase.  
 CAA82993.1 Z30332 *Spinacia oleracea*  
 protein kinase.  
 AAB88817.1 AF033263 *Zea mays*  
 signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat NPH1 proteins.

CAB65325.1 AJ252142 *Oryza sativa*  
 putative blue light receptor phototropin. non-phototropic hypocotyl NPH1. nph1.

CAA82994.1 Z30333 *Mesembryanthemum crystallinum*  
 protein kinase.

BAA36192.1 AB012082 *Adiantum capillus-veneris*  
 PHY3. PHY3. Ser/Thr protein kinase; chimeric structure of red/far-red light photoreceptive region (phytochrome)and putative blue light photoreceptor in phototropism of hypocotyl (NPH1).

SEQ ID NO: 446

AAB72047.1 AF006489 *Gossypium hirsutum*  
 adenine nucleotide translocator 1. CANT1.  
 CAA05979.1 AJ003197 *Lupinus albus*  
 transfer of ATP from mitochondria to cytosol. adenine nucleotide translocator. ant1.

CAA44054.1	X62123	Solanum tuberosum ADP /ATP translocator. ant. product has dimeric subunit structure.
AAB49700.1	U89839	Lycopersicon esculentum ADP/ATP translocator.
CAA40782.1	X57557	Solanum tuberosum adenine nucleotide translocator. AAC.
BAA02161.1	D12637	Oryza sativa ATP/ADP translocator.
CAA41812.1	X59086	Zea mays adenine nucleotide translocator. MANT2.
CAA40781.1	X57556	Zea mays adenine nucleotide translocator. MANT1.
CAA33743.1	X15712	Zea mays adenine nucleotide translocator.
CAA33742.1	X15711	Zea mays adenine nucleotide translocator.
CAA65119.1	X95863	Triticum turgidum adenine nucleotide translocator.
CAA26600.1	X02842	Zea mays put. ATP/ADP translocator.
CAA65120.1	X95864	Triticum turgidum adenine nucleotide translocator.
CAA46311.1	X65194	Chlamydomonas reinhardtii mitochondrial ADP/ATP translocator protein. CRANT.
AAA33027.1	M76669	Chlorella kessleri ATP/ADP translocator. AAT.
AAB72048.1	AF006490	Gossypium hirsutum adenine nucleotide translocator 2. CANT2.
BAA08104.1	D45074	Panicum miliaceum 2-oxoglutarate/malate translocator. mitochondrial 2-oxoglutarate/malate translocator.
BAA08103.1	D45073	Panicum miliaceum 2-oxoglutarate/malate translocator. mitochondrial 2-oxoglutarate/malate translocator.
BAA08105.1	D45075	Panicum miliaceum 2-oxoglutarate/malate translocator. mitochondrial 2-oxoglutarate/malate translocator.
SEQ ID NO: 447		
BAB16317.1	AB049589	Avicennia marina secretory peroxidase. PER.
AAC83463.1	AF039027	Glycine max H2O2 oxidoreductase. cationic peroxidase 2. Prx2. class III plant peroxidase.
AAD37374.1	AF145348	Glycine max peroxidase. Prx2b.

CAB71128.2	AJ271660	<i>Cicer arietinum</i> cationic peroxidase.
AAD33072.1	AF149251	<i>Nicotiana tabacum</i> secretory peroxidase. PER.
AAA99868.1	L08199	<i>Gossypium hirsutum</i> peroxidase. putative.
BAA94962.1	AB042103	<i>Asparagus officinalis</i> peroxidase. AspPOX1.
AAF63027.1	AF244924	<i>Spinacia oleracea</i> hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAF63026.1	AF244923	<i>Spinacia oleracea</i> hydrogen peroxide catabolism. peroxidase prx14 precursor. type III peroxidase.
BAA92500.1	AP001383	<i>Oryza sativa</i> ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
AAF63025.1	AF244922	<i>Spinacia oleracea</i> hydrogen peroxide catabolism. peroxidase prx13 precursor. type III peroxidase.
AAG46133.1	AC082644	<i>Oryza sativa</i> putative peroxidase. OSJNBa0013M12.15.
AAA32973.1	M73234	<i>Hordeum vulgare</i> peroxidase BP 1. Prx5.
CAA71493.1	Y10467	<i>Spinacia oleracea</i> peroxidase. prxr6.
AAG46122.1	AC082644	<i>Oryza sativa</i> putative peroxidase. OSJNBa0013M12.2.
AAG46141.1	AC082644	<i>Oryza sativa</i> putative peroxidase. OSJNBa0013M12.11.
BAA77387.1	AB024437	<i>Scutellaria baicalensis</i> peroxidase 1.
AAG46142.1	AC082644	<i>Oryza sativa</i> putative peroxidase. OSJNBa0013M12.9.
AAB02926.1	U59284	<i>Linum usitatissimum</i> peroxidase. FLXPER3.
CAA50597.1	X71593	<i>Lycopersicon esculentum</i> peroxidase. CEVI-1.
BAA82306.1	AB027752	<i>Nicotiana tabacum</i> peroxidase.
CAB67121.1	Y19023	<i>Lycopersicon esculentum</i> peroxidase. cevi-1.
AAG46125.1	AC082644	<i>Oryza sativa</i> putative peroxidase. OSJNBa0013M12.17.

BAA92422.1 AP001366 *Oryza sativa*  
ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene.  
Similar to *A.thaliana* mRNA for peroxidase ATP18a. (X98804).

BAA92497.1 AP001383 *Oryza sativa*  
ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene.  
Similar to peroxidase ATP18a. (X98804).

CAA59487.1 X85230 *Triticum aestivum*  
peroxidase. *pox4*.

AAA98491.1 L36981 *Petroselinum crispum*  
anionic peroxidase.

CAA71492.1 Y10466 *Spinacia oleracea*  
peroxidase. *prx5*.

BAA96643.1 AP002482 *Oryza sativa*  
Similar to *Arabidopsis thaliana* peroxidase ATP19a (X98805).

BAB12025.1 AP002820 *Oryza sativa*  
putative peroxidase. P0702D12.1.

AAB02554.1 L37790 *Stylosanthes humilis*  
cationic peroxidase.

AAF63024.1 AF244921 *Spinacia oleracea*  
hydrogen peroxide catabolism. peroxidase *prx12* precursor. type III peroxidase.

AAC84140.1 AF101427 *Cichorium intybus*  
peroxidase.

AAA65637.1 L13654 *Lycopersicon esculentum*  
peroxidase. *TPX1*.

AAC98519.1 AF007211 *Glycine max*  
peroxidase precursor. GMIPER1. pathogen-induced.

BAA14143.1 D90115 *Armoracia rusticana*  
peroxidase isozyme.

CAA62226.1 X90693 *Medicago sativa*  
peroxidase1B. *prx1B*.

AAD37430.1 AF149280 *Phaseolus vulgaris*  
peroxidase 5 precursor. FBP5. secretory peroxidase.

CAA62615.1 X91232 *Mercurialis annua*  
PRX. peroxidase.

AAG46130.1 AC082644 *Oryza sativa*  
putative peroxidase. OSJNBa0013M12.18.

CAC21392.1 AJ401275 *Zea mays*  
peroxidase. *pox2*.

BAA07241.1 D38051 *Populus kitakamiensis*  
peroxidase. *prxA4a*.

BAB39277.1 AP002971 *Oryza sativa*  
putative peroxidase. P0537A05.6. contains ESTs C23550(C52903),C97179(C52903).

CAB65334.1 AJ250121 *Picea abies*  
 peroxidase. SPI2 protein. spi2.

CAA62597.1 X91172 *Raphanus sativus*  
 korean-radish isoperoxidase. prxk1.

AAC49820.1 AF014469 *Oryza sativa*  
 peroxidase. POX5.1. wound inducible.

CAA71496.1 Y10470 *Spinacia oleracea*  
 peroxidase. prxr9.

BAA01950.1 D11337 *Vigna angularis*  
 peroxidase.

CAA71491.1 Y10465 *Spinacia oleracea*  
 peroxidase. prxr4.

BAA03911.1 D16442 *Oryza sativa*  
 peroxidase.

SEQ ID NO: 449

CAA56325.1 X80023 *Triticum turgidum*  
 ATP/ADP carrier protein.

CAC27140.1 AJ132535 *Picea abies*  
 ADP, ATP carrier protein precursor.

BAA92520.1 AP001383 *Oryza sativa*  
 ESTs AU068633(C30614),AU068634(C30614) correspond to a region of the predicted gene.  
 Similar to *Bos taurus* mitochondrial solute carrier protein. (AF049236).

BAB16462.1 AP002483 *Oryza sativa*  
 putative peroxisomal Ca-dependent solute carrier protein. P0019D06.21.

BAB40117.1 AP003311 *Oryza sativa*  
 putative peroxisomal Ca-dependent solute carrier protein. P0024G09.9.

AAB71744.1 U75346 *Chlamydomonas reinhardtii*  
 envelope protein. LIP-36G2. low CO<sub>2</sub> inducible carrier protein LIP-36 with a molecular weight of 36 kDa.

AAB71743.1 U75345 *Chlamydomonas reinhardtii*  
 envelope protein. LIP-36G1. low CO<sub>2</sub> inducible carrier protein LIP-36 with a molecular weight of 36 kDa.

AAG48999.1 AY013246 *Hordeum vulgare*  
 putative mitochondrial carrier protein. 635P2.1.

CAC12820.1 AJ299250 *Nicotiana tabacum*  
 mitochondrial 2-oxoglutarate/malate carrier protein. momc1.

CAA07568.1 AJ007580 *Ribes nigrum*  
 Mitochondrial carrier protein. prib7.

AAG45489.1 AY013245 *Oryza sativa*  
 36I5.1. putative mitochondrial carrier protein.

SEQ ID NO: 451

AAB53099.1 U68217 *Brassica napus*  
 iron binding protein. ferritin. LSC30.

AAA33959.1 M64337 Glycine max  
ferritin light chain. ferritin.

AAA34016.1 M72894 Glycine max  
ferritin light chain. SOF-H2.

CAA65771.1 X97059 Medicago sativa  
iron storage. ferritin. FER. abscissic acid regulated.

AAB18928.1 U31648 Glycine max  
iron storage protein. ferritin.

AAC06026.1 AF052057 Vigna unguiculata  
iron storage and mobilization in plants. ferritin subunit cowpea3 precursor.

AAC06027.1 AF052058 Vigna unguiculata  
iron storage and mobilization in plants. ferritin subunit cowpea2 precursor.

CAA41213.1 X58274 Phaseolus vulgaris  
ferritin. pfe.

AAD50644.1 AF133814 Solanum tuberosum  
ferritin 1. F1.

CAA51786.1 X73369 Pisum sativum  
ferritin.

CAA45763.1 X64417 Pisum sativum  
ferritin-precursor.

CAA43663.1 X61391 Zea mays  
ferritin.

CAA58146.1 X83076 Zea mays  
ferritin. Fer1.

CAA58147.1 X83077 Zea mays  
ferritin. Fer2.

CAA43664.1 X61392 Zea mays  
ferritin.

AAA33958.1 M58336 Glycine max  
ferritin light chain. SOF-5L.

CAB42587.1 AJ238628 Chlorella protothecoides  
putative ferritin. dee188.

BAB17852.1 AB042612 Nicotiana tabacum  
ferritin 1. tob-fer-1. putative.

AAC15241.1 AF028072 Pinus taeda  
ferritin.

CAA47982.1 X67754 Vigna unguiculata  
ferritin 1. pfe1.

CAA47984.1 X67756 Vigna unguiculata  
ferritin 5. pfe5.

CAA47983.1 X67755 Vigna unguiculata  
ferritin 2. pfe2.

AAC12282.1	AF052511	Glycine max iron storage and mobilization. ferritin 2. soybean 2; cowpea 2 homolog.
AAC12281.1	AF052513	Glycine max iron storage and mobilization. ferritin 1. soybean 1; cowpea 1 homolog.
		SEQ ID NO: 452
CAB56619.1	AJ244024	Nicotiana tabacum putative role in cell plate formation. phragmoplastin. phragmoplastin. dynamin-like protein.
		SEQ ID NO: 454
CAA55039.1	X78203	Hyoscyamus muticus glutathione transferase.
AAB65163.1	AF002692	Solanum commersonii glutathione S-transferase, class-phi. GST1. low temperature induced.
BAA01394.1	D10524	Nicotiana tabacum glutathione S-transferase. parB.
CAA96431.1	Z71749	Nicotiana plumbaginifolia glutathione S-transferase.
AAA33931.1	M84969	Silene vulgaris glutathione-S-transferase.
AAA33930.1	M84968	Silene vulgaris glutathione-S-transferase.
AAF65767.1	AF242309	Euphorbia esula glutathione S-transferase. putative auxin-binding GST.
AAF61392.1	AF133894	Persea americana glutathione S-transferase. GTH.
CAB38119.1	AJ010296	Zea mays Glutathione transferase III(b). gst3b.
CAB38118.1	AJ010295	Zea mays Glutathione transferase III(a). gst3a.
BAB39935.1	AP002914	Oryza sativa putative glutathione S-transferase. P0493G01.17.
AAG34811.1	AF243376	Glycine max glutathione S-transferase GST 21.
BAB39939.1	AP002914	Oryza sativa putative glutathione S-transferase. P0493G01.21.
AAG34812.1	AF243377	Glycine max glutathione S-transferase GST 22.
AAG34814.1	AF243379	Glycine max glutathione S-transferase GST 24.
CAA09190.1	AJ010451	Alopecurus myosuroides glutathione transferase. GST2a.
AAG32476.1	AF309383	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTF4.

BAB39929.1 AP002914 *Oryza sativa*  
putative glutathione transferase. P0493G01.7.

CAA09193.1 AJ010454 *Alopecurus myosuroides*  
glutathione transferase. GST2d.

BAB39941.1 AP002914 *Oryza sativa*  
putative glutathione S-transferase. P0493G01.23.

CAA09191.1 AJ010452 *Alopecurus myosuroides*  
glutathione transferase. GST2b.

CAA09192.1 AJ010453 *Alopecurus myosuroides*  
glutathione transferase. GST2c.

AAD56395.1 AF184059 *Triticum aestivum*  
glutathione S-transferase. GST1.

CAA39487.1 X56012 *Triticum aestivum*  
glutathione transferase. gstA1.

AAG32477.1 AF309384 *Oryza sativa* subsp. *japonica*  
putative glutathione S-transferase OsGSTF3.

CAA68993.1 Y07721 *Petunia x hybrida*  
conjugates glutathione to anthocyanin to facilitate transport to the vacuole. glutathione S-transferase. an9 locus.

AAA33470.1 M16901 *Zea mays*  
glutathione S-transferase I.

AAA33469.1 M16902 *Zea mays*  
glutathione S-transferase I.

AAA20585.1 U12679 *Zea mays*  
glutathione S-transferase IV. GSTIV.

CAA56047.1 X79515 *Zea mays*  
glutathione transferase. GST27.

CAB66333.1 AJ279691 *Betula pendula*  
glutathione-S-transferase. gst.

BAB39927.1 AP002914 *Oryza sativa*  
putative glutathione S-transferase. P0493G01.1. contains ESTs  
AU031696(R0596), C97559(C60386), C28218(C60386), D28287(R0596).

AAC64007.1 AF062403 *Oryza sativa*  
glutathione S-transferase II.

CAA39480.1 X56004 *Triticum aestivum*  
glutathione transferase. gstA2.

AAG32475.1 AF309382 *Oryza sativa* subsp. *japonica*  
putative glutathione S-transferase OsGSTF5.

AAG34823.1 AF244680 *Zea mays*  
glutathione S-transferase GST 15.

BAB39940.1 AP002914 *Oryza sativa*  
putative glutathione S-transferase. P0493G01.22.

AAG34818.1 AF244675 Zea mays  
glutathione S-transferase GST 10.

AAG34820.1 AF244677 Zea mays  
glutathione S-transferase GST 11.

AAG34817.1 AF244674 Zea mays  
glutathione S-transferase GST 9.

AAG34821.1 AF244678 Zea mays  
glutathione S-transferase GST 13.

CAA05354.1 AJ002380 Oryza sativa  
glutathione S-transferase. Rgst I.

AAG34816.1 AF244673 Zea mays  
glutathione S-transferase GST 8.

AAG34822.1 AF244679 Zea mays  
glutathione S-transferase GST 14.

CAA05355.1 AJ002381 Oryza sativa  
glutathione S-transferase. Rgst II.

SEQ ID NO: 458

AAD45623.1 AF084185 Brassica napus  
dehydration responsive element binding protein. DNA binding protein; DRE binding protein.

BAA90812.1 AP001168 Oryza sativa  
Similar to mRNA for DREB1A (AB007787).

AAK01089.1 AF298231 Hordeum vulgare  
CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.

AAG59618.1 AF239616 Hordeum vulgare  
CRT/DRE-binding factor. CBF.

AAK01088.1 AF298230 Hordeum vulgare  
CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.

AAG59619.1 AF243384 Oryza sativa  
CRT/DRE binding factor. CBF. DREB.

AAC29516.1 U77655 Solanum tuberosum  
DNA binding protein homolog. STWAAEIRD.

BAA76734.1 AB024575 Nicotiana tabacum  
ethylene responsive element binding factor.

CAB93939.1 AJ238739 Catharanthus roseus  
putative transcription factor. AP2-domain DNA-binding protein. orcal.

BAB03248.1 AB037183 Oryza sativa  
ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.

BAA97123.1 AB016265 Nicotiana sylvestris  
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.

BAA97124.1 AB016266 Nicotiana sylvestris  
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

AAC50047.1 U89255 *Lycopersicon esculentum*  
binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pt14.

AAD00708.1 U91857 *Stylosanthes hamata*  
ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4  
proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125  
respectively.

AAC14323.1 AF058827 *Nicotiana tabacum*  
TSI1. Ts1. contains putative AP2 DNA-binding domain; similar to Pt16.

AAG60182.1 AC084763 *Oryza sativa*  
putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

AAK31279.1 AC079890 *Oryza sativa*  
putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

AAC49741.1 U89257 *Lycopersicon esculentum*  
DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pt16.

BAA97122.1 AB016264 *Nicotiana sylvestris*  
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related)  
gene of higher plant. ethylene-responsive element binding factor. nserf2.

CAB96900.1 AJ251250 *Catharanthus roseus*  
transcription factor. AP2-domain DNA-binding protein. orca3.

CAB96899.1 AJ251249 *Catharanthus roseus*  
transcription factor. AP2-domain DNA-binding protein. orca3.

BAB21218.1 AP002913 *Oryza sativa*  
putative DNA binding protein RAV2. P0480E02.24.

CAB93940.1 AJ23S740 *Catharanthus roseus*  
putative transcription factor. AP2-domain DNA-binding protein. orca2.

BAA87068.1 AB035270 *Matricaria chamomilla*  
ethylene-responsive element binding protein1 homolog. McEREBP1.

AAC49740.1 U89256 *Lycopersicon esculentum*  
binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pt15.

AAB38748.1 U81157 *Nicotiana tabacum*  
S25-XP1 DNA binding protein.

BAB21211.1 AP002913 *Oryza sativa*  
putative DNA binding protein RAV2. P0480E02.17.

BAA78732.1 AB023482 *Oryza sativa*  
Similar to *Arabidopsis thaliana* mRNA for DREB1B, complete cds.(AB007788).

SEQ ID NO: 460

AAB67721.1 AF015269 *Zea mays*  
PL transcription factor. Pl. nonfunctional due to retrotransposon insertion.

SEQ ID NO: 461

AAD50592.1 AF093752 *Triticum aestivum*  
phytochelatin synthase. PCS1.

AAG22095.1 AF308658 *Typha latifolia*  
phytochelatin synthase.

## SEQ ID NO: 463

AAG13629.1 AC078840 Oryza sativa  
putative steroid membrane binding protein. OSJNBb0073N24.4.

AAG13623.1 AC078840 Oryza sativa  
putative steroid membrane binding protein. OSJNBb0073N24.2.

## SEQ ID NO: 464

CAA56313.1 X79992 Avena sativa  
putative pp70 ribosomal protein S6 kinase. Aspk11.

CAB89082.1 AJ277534 Asparagus officinalis  
S6 ribosomal protein kinase. pk1. putative.

AAK18843.1 AC082645 Oryza sativa  
putative protein kinase. OSJNBb0033N16.3.

AAC05083.1 AF033096 Avena sativa  
NPH1-1. NPH1-1. putative serine/threonine protein kinase.

AAC05084.1 AF033097 Avena sativa  
NPH1-2. NPH1-2. putative serine/threonine protein kinase.

AAK13156.1 AC078829 Oryza sativa  
putative protein kinase. OSJNBa0026O12.14.

CAB82852.1 Z30329 Mesembryanthemum crystallinum  
protein kinase MK6.

AAB88817.1 AF033263 Zea mays  
signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat NPH1 proteins.

BAB18105.1 AB042715 Chlamydomonas reinhardtii  
cyclic nucleotide dependent protein kinase II. CL-PK2.

BAB18104.1 AB042714 Chlamydomonas reinhardtii  
cyclic nucleotide dependent protein kinase. CL-PK1.

BAA83689.1 AB011968 Oryza sativa  
OsPK7. OsPK7. protein kinase.

BAA92970.1 AP001551 Oryza sativa  
Similar to Arabidopsis thaliana chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).

AAD31900.1 AF145482 Mesembryanthemum crystallinum  
putative serine/threonine protein kinase.

BAA92972.1 AP001551 Oryza sativa  
ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene.  
Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase.  
(AL022198).

BAA83688.1 AB011967 Oryza sativa  
OsPK4. OsPK4. protein kinase.

CAA73067.1 Y12464 Sorghum bicolor  
serine/threonine kinase. SNFL1.

AAF22219.1 AF141378 *Zea mays*  
protein kinase PK4. ZmPK4.

BAA96628.1 AP002482 *Oryza sativa*  
ESTs D41739(S4522),AU055999(S20214), AU057588(S21592 correspond to a region of the  
predicted gene. Similar to *Sorghum bicolor* serine/threonine kinase (Y12465).

CAA89202.1 Z49233 *Chlamydomonas eugametos*  
calcium-stimulated protein kinase.

CAA73068.1 Y12465 *Sorghum bicolor*  
serine/threonine kinase. SNFL2.

BAA34675.1 AB011670 *Triticum aestivum*  
wpk4 protein kinase. wpk4.

BAA99439.1 AP002743 *Oryza sativa*  
putative protein kinase. P0710E05.26. contains ESTs C22394(C30013),C22393(C30013).

CAA74646.1 Y14274 *Sorghum bicolor*  
putative serine/threonine protein kinase. SNFL3.

BAB12687.1 AP002746 *Oryza sativa*  
putative protein kinase. P0671B11.2. contains ESTs C22394(C30013),C22393(C30013).

AAF06969.1 AF162661 *Kalanchoe fedtschenkoi*  
phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.

AAF06970.1 AF162662 *Kalanchoe fedtschenkoi*  
phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.

BAA90814.1 AP001168 *Oryza sativa*  
ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.;  
Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).

AAB62693.1 AF004947 *Oryza sativa*  
protein kinase.

AAF21062.1 AF216527 *Dunaliella tertiolecta*  
calcium-dependent protein kinase. CPK1; CDPK.

CAA71142.1 Y10036 *Cucumis sativus*  
SNF1-related protein kinase.

CAA39936.1 X56599 *Daucus carota*  
calcium- dependent protein kinase. DcPK431.

CAA08995.1 AJ010091 *Brassica napus*  
MAP3K alpha 1 protein kinase. MAP3K alpha 1.

BAA05649.1 D26602 *Nicotiana tabacum*  
protein kinase.

AAF19403.1 AF203481 *Lycopersicon esculentum*  
phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase  
family; lacks the autoinhibitory region and EF hands.

AAC25423.1 AF072908 *Nicotiana tabacum*  
calcium-dependent protein kinase. CDPK1.

AAF19402.1 AF203480 *Lycopersicon esculentum*  
 phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.

CAA65244.1 X95997 *Solanum tuberosum*  
 SNF1-related protein kinase. PKIN1.

CAA57898.1 X82548 *Hordeum vulgare*  
 SNF1-related protein kinase. BKIN2.

AAF19401.1 AF203479 *Glycine max*  
 phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.

AAD23582.1 AF128443 *Glycine max*  
 probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.

AAF34436.1 AF172282 *Oryza sativa*  
 similar to mitogen-activated protein kinases. DUPR11.32.

BAA05648.1 D26601 *Nicotiana tabacum*  
 protein kinase.

SEQ ID NO: 465

CAB85467.1 AJ250316 *Brassica juncea*  
 chloroplast omega-3 fatty acid desaturase. fad7.

BAA22441.1 D63954 *Zea mays*  
 fatty acid desaturase. FAD7.

BAA11475.1 D79979 *Nicotiana tabacum*  
 omega-3 fatty acid desaturase. NtFAD7.

AAA70334.1 U25817 *Sesamum indicum*  
 omega-3 fatty acid desaturase. linoleic acid and hexadecadienoic acids desaturase.

AAB39387.1 U59477 *Perilla frutescens*  
 omega-3 fatty acid desaturase.

CAA07638.1 AJ007739 *Solanum tuberosum*  
 w-3 desaturase.

AAF27933.1 AF222989 *Capsicum annuum*  
 omega-3 fatty acid desaturase. FAD.

AAB72241.1 U75745 *Petroselinum crispum*  
 omega-3 fatty acid desaturase. complements the *Arabidopsis fad7/8* fatty acid double mutant.

AAA61776.1 L22965 *Chloroplast Glycine soja*  
 omega-3 fatty acid desaturase. Fadd.

AAF12821.1 AF200717 *Vernicia fordii*  
 TnDES2. omega-3 fatty acid desaturase.

AAA86690.1 U17063 *Limnanthes douglasii*  
 linoleic acid desaturation. delta-15 lineoyl desaturase. omega-3-fatty acid desaturase.

AAA73511.1 L25897 *Ricinus communis*  
 desaturates linoleate to alpha-linolenate. linoleoyl desaturase. fad7. putative.

CAC18722.1 AJ302017 *Picea abies*  
putative plastidial w-3 fatty acid desaturase. fad3.

AAD13527.1 AF061027 *Vernicia fordii*  
omega-3 fatty acid desaturase precursor.

BAA22442.1 D84409 *Zea mays*  
fatty acid desaturase. FAD8.

BAA22440.1 D63953 *Zea mays*  
fatty acid desaturase. FAD8.

BAA07785.2 D43688 *Triticum aestivum*  
plastid omega-3 fatty acid desaturase. TaFAD7.

AAA61774.1 L22963 *Chloroplast Brassica napus*  
omega-3 fatty acid desaturase. Fadd.

AAC98967.1 AF047172 *Vernicia fordii*  
omega-3 fatty acid desaturase. Fad3.

CAB45155.1 AJ011004 *Vernicia fordii*  
omega-3 desaturase.

AAC16443.1 AF020204 *Pelargonium x hortorum*  
omega-3 desaturase. pxh-15.

AAA61775.1 L22962 *Brassica napus*  
omega-3 fatty acid desaturase. Fad3.

AAA61777.1 L22964 *Chloroplast Glycine soja*  
omega-3 fatty acid desaturase. Fad3.

AAA32994.1 L01418 *Brassica napus*  
desaturation of linoleic acid to linolenic acid. linoleic acid desaturase. fad3.

AAD15744.1 AF047039 *Perilla frutescens*  
omega-3 fatty acid desaturase. FAD3.

BAA28358.1 D84678 *Triticum aestivum*  
omega-3 fatty acid desaturase. TaFAD3.

BAA05515.1 D26509 *Nicotiana tabacum*  
desaturation of dienoic fatty acid. microsomal omega-3 acid desaturase. NtFAD3.

BAA11397.1 D78506 *Oryza sativa*  
w-3 fatty acid desaturase.

BAB18135.1 AB051215 *Glycine max*  
microsomal omega-3 fatty acid desaturase.

BAA22439.1 D63952 *Zea mays*  
fatty acid desaturase. FAD7.

BAA11396.1 D78505 *Oryza sativa*  
w-3 fatty acid desaturase.

CAB71341.1 AJ250664 *Hordeum vulgare*  
omega-3 fatty acid desaturase. bci-8.

AAD48897.1 AF083613 *Dunaliella salina*  
omega-3 fatty acid desaturase. des3-1.

AAF80560.1 AF192486 *Sesamum indicum*  
omega-6 fatty acid desaturase. FAD2.

CAB64256.1 AJ245938 *Calendula officinalis*  
production of calendic acid. (8,11)-linoleoyl desaturase. des8.11.

AAB80696.1 U86072 *Petroselinum crispum*  
omega-6 fatty acid desaturase. functional expression in yeast results in the formation of  
dienoic fatty acids (18:2 and 16:2).

SEQ ID NO: 467

CAA60016.1 X86021 *Solanum tuberosum*  
potassium channel. SKT1 gene. putative start codon.

CAA65254.1 X96390 *Lycopersicon esculentum*  
potassium channel. LKT1.

AAF36832.1 AF207745 *Triticum aestivum*  
AKT1-like potassium channel. TaAKT1.

CAA68912.1 Y07632 *Zea mays*  
potassium channel. ZMK1.

AAF81249.1 AF267753 *Mesembryanthemum crystallinum*  
putative potassium channel protein Mkt1p.

CAC05489.1 AJ271447 *Populus tremula x Populus tremuloides*  
potassium channel. potassium channel 2. ptk2.

AAD16278.1 AF099095 *Samanea saman*  
pulvinus inward-rectifying channel for potassium SPICK1. similar to *Arabidopsis* potassium  
channel AKT3.

CAB54856.1 AJ132686 *Zea mays*  
potassium channel protein ZMK2. ZMK2.

CAA70870.1 Y09699 *Solanum tuberosum*  
putative inward rectifying potassium channel. SKT2.

CAA71598.1 Y10579 *Vicia faba*  
potassium channel.

BAA84085.1 AB032074 *Nicotiana paniculata*  
potassium channel. NpKT1.

CAA12645.1 AJ225805 *Egeria densa*  
inward potassium channel alpha subunit. homologous to the sequences of the family of  
inwardly rectifying potassium channels in plants which is structurally related to the shaker  
family of outwardly rectifying channels in *Drosophila*.

AAD39492.1 AF145272 *Samanea saman*  
pulvinus inward-rectifying channel SPICK2. potassium channel; similar to AKT2/3.

CAC10514.1 AJ299019 *Samanea saman*  
potassium release. outwardly rectifying potassium channel. spork1.

CAC05488.1 AJ271446 *Populus tremula x Populus tremuloides*  
potassium channel. outward rectifying potassium channel. ptork.

AAF81251.1 AF267755 *Mesembryanthemum crystallinum*  
potassium channel protein Mkt2p.

CAA70900.1	Y09753	Secale cereale
<u>potassium channel. encodes membrane spanning domains H5-S6.</u>		
CAA70899.1	Y09752	Secale cereale
<u>potassium channel. encodes membrane spanning domains H5-S6.</u>		
CAA70947.1	Y09818	Solanum tuberosum
<u>putative inward rectifying potassium channel. SKT3.</u>		
CAA70895.1	Y09748	Hordeum vulgare
<u>potassium channel. encodes membrane spanning domains H5-S6.</u>		
CAA70894.1	Y09747	Zea mays
<u>potassium channel. encodes membrane spanning domains H5-S6.</u>		
CAA70896.1	Y09749	Vicia faba
<u>potassium channel. encodes membrane spanning domains H5-S6.</u>		
CAA70897.1	Y09750	Plantago major
<u>potassium channel. encodes membrane spanning domains H5-S6.</u>		
AAF33670.1	AF079872	Nicotiana tabacum
<u>cyclic nucleotide-gated calmodulin-binding ion channel. CBP4.</u>		
AAF33669.1	AF079871	Nicotiana tabacum
<u>cyclic nucleotide-gated calmodulin-binding ion channel. CBP7.</u>		
CAA05637.1	AJ002610	Hordeum vulgare
<u>putative calmodulin binding transporter protein. CBT1.</u>		
CAA70898.1	Y09751	Plantago major
<u>potassium channel. encodes membrane spanning domains H5-S6.</u>		
AAK16188.1	AC079887	Oryza sativa
<u>putative cyclic nucleotide and calmodulin-regulated ion channel protein. OSJNBA0040E01.13.</u>		
SEQ ID NO: 468		
AAF76226.1	AF272572	Populus x canescens
<u>14-3-3 protein. 14-3-3P20-1.</u>		
AAC04811.1	AF037460	Fritillaria agrestis
<u>GF14 protein. GRF.</u>		
AAB40395.1	U80070	Mesembryanthemum crystallinum
<u>G-box binding factor. 14-3-3-like protein. GBF.</u>		
AAF05737.1	AF191746	Lilium longiflorum
<u>14-3-3-like protein.</u>		
AAB07457.1	U65957	Oryza sativa
<u>GF14-c protein. rice 14-3-3 protein homolog; osGF14c.</u>		
AAB09580.1	U70533	Glycine max
<u>SGF14A. 14-3-3 related protein.</u>		
AAA99431.1	L29150	Lycopersicon esculentum
<u>14-3-3 protein homologue.</u>		
CAA74592.1	Y14200	Hordeum vulgare
<u>14-3-3 protein.</u>		

AAB33304.1	S77133	Zea mays
GF14-6. GRF1. 14-3-3 protein homolog; This sequence comes from Fig. 5.		
CAA66309.1	X97724	Solanum tuberosum
14-3-3 protein. leaf specific.		
AAB07456.1	U65956	Oryza sativa
GF14-b protein. rice 14-3-3 protein homolog; osGF14b.		
AAD27823.2	AF121194	Populus x canescens
14-3-3 protein. 14-3-3P20-2.		
AAC49894.1	U91726	Nicotiana tabacum
14-3-3 isoform e. T14-3e.		
CAA44259.1	X62388	Hordeum vulgare
14-3-3 protein homologue.		
AAD27827.2	AF121198	Picea glauca
14-3-3 protein. 14-3-3EB9D.		
CAA63658.1	X93170	Hordeum vulgare
Hv14-3-3b.		
CAB42546.2	AJ238681	Pisum sativum
14-3-3-like protein. 14-3-3.		
AAA33505.1	M96856	Zea mays
regulatory protein. GF14-12.		
AAA85817.1	U15036	Pisum sativum
14-3-3-like protein.		
AAK26634.1	AF342780	Brassica napus
GF14 omega. 14-3-3 protein.		
CAA72094.1	Y11211	Nicotiana tabacum
14-3-3-like protein B.		
CAA72383.1	Y11687	Solanum tuberosum
14-3-3 protein. 34G.		
AAC49892.1	U91724	Nicotiana tabacum
14-3-3 isoform c. T14-3c.		
CAA53700.1	X76086	Cucurbita pepo
14-3-3 protein 32kDa endonuclease. A215. single polypeptide.		
CAA72382.1	Y11686	Solanum tuberosum
14-3-3 protein. 30G.		
CAB42547.1	AJ238682	Pisum sativum
14-3-3-like protein. 14-3-3.		
CAA65147.1	X95902	Lycopersicon esculentum
14-3-3 protein. tft3 gene.		
AAC49891.1	U91723	Nicotiana tabacum
14-3-3 isoform b. T14-3b.		
AAB07458.1	U65958	Oryza sativa
GF14-d protein. rice 14-3-3 protein homolog; osGF14d.		

CAA72381.1	Y11685	Solanum tuberosum
14-3-3 protein. 16R.		
AAC49895.1	U91727	Nicotiana tabacum
14-3-3 isoform f. T14-3f.		
CAA72095.1	Y11212	Nicotiana tabacum
14-3-3-like protein A.		
BAB11739.1	AB042193	Triticum aestivum
TaWIN1. TaWIN1. TaWIN1 is a member of 14-3-3 protein family.		
CAA65146.1	X95901	Lycopersicon esculentum
14-3-3 protein. tft2 gene.		
CAA65148.1	X95903	Lycopersicon esculentum
14-3-3 protein. tft5 gene.		
AAC17447.1	AF066076	Helianthus annuus
14-3-3-like protein.		
CAA60800.1	X87370	Solanum tuberosum
14-3-3 protein. RA215. root specific.		
CAA55964.1	X79445	Chlamydomonas reinhardtii
14-3-3 protein.		
CAC03467.1	Y19105	Chlamydomonas reinhardtii
14-3-3 protein.		
CAA65149.1	X95904	Lycopersicon esculentum
14-3-3 protein. tft6 gene.		
CAB65693.1	AJ270959	Lycopersicon esculentum
tft3 14-3-3 protein. tft3.		
BAB11740.1	AB042194	Triticum aestivum
TaWIN2. TaWIN2. TaWIN2 is a member of 14-3-3 protein family.		
AAA99430.1	L29151	Lycopersicon esculentum
14-3-3 protein homologue.		
CAA72384.1	Y11688	Solanum tuberosum
14-3-3 protein. 35G.		
CAA65145.1	X95900	Lycopersicon esculentum
14-3-3 protein. tft1 gene.		
AAC49893.1	U91725	Nicotiana tabacum
14-3-3 isoform d. T14-3d.		
SEQ ID NO: 470		
AAA19701.1	L24438	Thlaspi arvense
cytochrome P450.		
AAA32913.1	M32885	Persea americana
cytochrome P-450LXXIA1 (cyp71A1).		
AAC39318.1	AF029858	Sorghum bicolor
second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldioxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.		

BAB40323.1	AB037244	Asparagus officinalis cytochrome P450. ASPI-1.
BAB40324.1	AB037245	Asparagus officinalis cytochrome P450. ASPI-2.
AAB94589.1	AF022460	Glycine max CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
CAA70576.1	Y09424	Nepeta racemosa cytochrome P450. CYP71A6.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
AAB61965.1	U48435	Solanum chacoense putative cytochrome P450.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
CAA50312.1	X70981	Solanum melongena P450 hydroxylase. CYPEG2.
CAA71514.1	Y10490	Glycine max putative cytochrome P450.
AAB94584.1	AF022157	Glycine max capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
AAD47832.1	AF166332	Nicotiana tabacum cytochrome P450.
AAF27282.1	AF122821	Capsicum annuum cytochrome P450. PepCYP.
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
CAA83941.1	Z33875	Mentha x piperita cytochrome P-450 oxidase.
CAB56503.1	AJ238612	Catharanthus roseus cytochrome P450.
AAB61964.1	U48434	Solanum chacoense putative cytochrome P450.
AAB69644.1	AF000403	Lotus japonicus putative cytochrome P450. LjNP450.
CAA50645.1	X71654	Solanum melongena P450 hydroxylase.
BAA03635.1	D14990	Solanum melongena Cytochrome P-450EG4.
AAD44151.1	AF124816	Mentha x piperita cytochrome p450 isoform PM17.

AAD44150.1 AF124815 *Mentha spicata*  
cytochrome p450.

AAD44152.1 AF124817 *Mentha x piperita*  
cytochrome p450 isoform PM2.

BAB39252.1 AP002968 *Oryza sativa*  
putative cytochrome P450. P0416G11.1.

AAK38084.1 AF321860 *Lolium rigidum*  
putative cytochrome P450.

AAK38083.1 AF321859 *Lolium rigidum*  
putative cytochrome P450.

AAK38087.1 AF321863 *Lolium rigidum*  
putative cytochrome P450.

AAK38082.1 AF321858 *Lolium rigidum*  
putative cytochrome P450.

CAC27827.1 AJ295719 *Catharanthus roseus*  
geraniol hydroxylase. cytochrome P450. cyp71.

AAB94587.1 AF022458 *Glycine max*  
CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

AAK38088.1 AF321864 *Lolium rigidum*  
putative cytochrome P450.

AAD37433.1 AF150881 *Lycopersicon esculentum x Lycopersicon peruvianum*  
catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase.  
CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.

AAG14963.1 AF214009 *Brassica napus*  
cytochrome p450-dependent monooxygenase. BNF5H3.

CAA57425.1 X81831 *Zea mays*  
cytochrome P450. CYP71C4. family CYP71, subfamily CYP71C.

CAA72196.1 Y11368 *Zea mays*  
cytochrome p450. cyp71c4.

AAG44132.1 AF218296 *Pisum sativum*  
cytochrome P450. P450 isolog.

AAG14962.1 AF214008 *Brassica napus*  
cytochrome p450-dependent monooxygenase. BNF5H2.

AAG14961.1 AF214007 *Brassica napus*  
cytochrome p450-dependent monooxygenase. BNF5H1.

AAD56282.1 AF155332 *Petunia x hybrida*  
flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

SEQ ID NO: 471

AAD17855.1 AF099111 *Zea mays*  
sigma factor. sig2. putative sigma subunit of chloroplast Escherichia coli-like RNA  
polymerase; Sig2.

SEQ ID NO: 472

AAD45623.1	AF084185	Brassica napus dehydration responsive element binding protein. DNA binding protein; DRE binding protein.
AAG43549.1	AF211531	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
AAG43548.1	AF211530	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
AAK01089.1	AF298231	Hordeum vulgare CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
AAG59618.1	AF239616	Hordeum vulgare CRT/DRE-binding factor. CBF.
AAK01088.1	AF298230	Hordeum vulgare CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
AAG59619.1	AF243384	Oryza sativa CRT/DRE binding factor. CBF. DREB.
AAK31271.1	AC079890	Oryza sativa putative transcriptional factor. OSJNBb0089A17.22.
CAC12822.1	AJ299252	Nicotiana tabacum AP2 domain-containing transcription factor. ap2.
BAA76734.1	AB024575	Nicotiana tabacum ethylene responsive element binding factor.
AAC29516.1	U77655	Solanum tuberosum DNA binding protein homolog. STWAAEIRD.
AAF23899.1	AF193803	Oryza sativa transcription factor EREBP1. EREBP/AP2-like transcription factor.
CAB93939.1	AJ238739	Catharanthus roseus putative transcription factor. AP2-domain DNA-binding protein. orca1.
BAB16083.1	AB036883	Oryza sativa transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.
BAB03248.1	AB037183	Oryza sativa ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
BAA97124.1	AB016266	Nicotiana sylvestris ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
BAA97123.1	AB016265	Nicotiana sylvestris ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
AAG43545.1	AF211527	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
AAD00708.1	U91857	Stylosanthes hamata ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

AAC49741.1	U89257	Lycopersicon esculentum DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pt16.
AAG60182.1	AC084763	Oryza sativa putative ethylene-responsive element binding protein. OSJNBA0027P10.12.
AAK31279.1	AC079890	Oryza sativa putative ethylene-responsive element binding protein. OSJNBB0089A17.16.
AAC14323.1	AF058827	Nicotiana tabacum TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pt16.
AAC50047.1	U89255	Lycopersicon esculentum binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pt14.
BAA97122.1	AB016264	Nicotiana sylvestris ERF (EREFP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
CAB96899.1	AJ251249	Catharanthus roseus transcription factor. AP2-domain DNA-binding protein. orca3.
CAB93940.1	AJ238740	Catharanthus roseus putative transcription factor. AP2-domain DNA-binding protein. orca2.
AAF63205.1	AF245119	Mesembryanthemum crystallinum AP2-related transcription factor. CDBP. stress induced transcription factor.
BAA87068.1	AB035270	Matricaria chamomilla ethylene-responsive element binding protein1 homolog. McEREBP1.
CAB96900.1	AJ251250	Catharanthus roseus transcription factor. AP2-domain DNA-binding protein. orca3.
BAB21218.1	AP002913	Oryza sativa putative DNA binding protein RAV2. P0480E02.24.
BAA07321.1	D38123	Nicotiana tabacum ERF1. ethylene-responsive transcription factor.
AAC49740.1	U89256	Lycopersicon esculentum binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pt15.
AAB38748.1	U81157	Nicotiana tabacum S25-XP1 DNA binding protein.
BAB21211.1	AP002913	Oryza sativa putative DNA binding protein RAV2. P0480E02.17.
SEQ ID NO: 473		
BAA85438.1	AP000616	Oryza sativa similar to RING-H2 finger protein RHA1a (AF078683).
AAK00436.1	AC060755	Oryza sativa putative zinc finger protein. OSJNBA0003O19.23.
AAG43550.1	AF211532	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.
SEQ ID NO: 475		
AAG43550.1	AF211532	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

BAA78746.1	AB023482	Oryza sativa
Similar to <i>Arabidopsis thaliana</i> RING-H2 finger protein RHX1a mRNA, partial cds.(AF079184).		
BAA96875.1	AB045121	Oryza sativa
RING finger 1. RRF1.		
CAA74911.1	Y14573	Hordeum vulgare
ring finger protein. putative.		
AAK00436.1	AC060755	Oryza sativa
putative zinc finger protein. OSJNBa0003O19.23.		
AAG46117.1	AC073166	Oryza sativa
putative ring finger protein. OSJNBb0064P21.7.		
BAA90357.1	AP001080	Oryza sativa
EST AU070319(S10788) corresponds to a region of the predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).		
BAA77204.1	AB026262	Cicer arietinum
ring finger protein.		
BAA90806.1	AP001168	Oryza sativa
ESTs C26000(C11448),AU082130(C11448) correspond to a region of the predicted gene.; Similar to mRNA for zinc-finger protein (Z36749).		
SEQ ID NO: 476		
BAA78764.1	AB023482	Oryza sativa
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to <i>Arabidopsis thaliana</i> APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).		
AAK11674.1	AF339747	Lophopyrum elongatum
protein kinase. ESI47.		
AAF43496.1	AF131222	Lophopyrum elongatum
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.		
AAG16628.1	AY007545	Brassica napus
protein serine/threonine kinase BNK1.		
BAA94509.1	AB041503	Populus nigra
protein kinase 1. PnPK1.		
BAA94510.1	AB041504	Populus nigra
protein kinase 2. PnPK2.		
BAB07999.1	AP002525	Oryza sativa
putative protein kinase. P0462H08.22. contains EST C22619(S11214).		
BAB03429.1	AP002817	Oryza sativa
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).		
BAA87853.1	AP000816	Oryza sativa
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).		

BAB16871.1 AP002537 *Oryza sativa*  
putative protein kinase APK1A *Arabidopsis thaliana*. P0001B06.24. contains ESTs  
C22608(R3192),D25110(R3192).

BAB39409.1 AP002901 *Oryza sativa*  
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

AAK00425.1 AC069324 *Oryza sativa*  
Putative protein kinase. OSJNBa0071K19.11.

BAB39873.1 AP002882 *Oryza sativa*  
putative protein kinase. P0439B06.8. contains ESTs  
AU056701(S20808),AU056702(S20808).

CAB51834.1 00069 *Oryza sativa*  
I1332.5. contains eukaryotic protein kinase domain PF.

BAB21240.1 AP002953 *Oryza sativa*  
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

AAK21965.1 AY028699 *Brassica napus*  
receptor protein kinase PERK1.

AAG59657.1 AC084319 *Oryza sativa*  
putative protein kinase. OSJNBa0004B24.20.

AAG03090.1 AC073405 *Oryza sativa*  
Similar to an *Arabidopsis* somatic embryogenesis receptor-like kinase (AC007504).

AAG25966.1 AF302082 *Nicotiana tabacum*  
cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly  
after cytokinin treatment.

BAB21241.1 AP002953 *Oryza sativa*  
Putative Pto kinase interactor 1. P0426D06.21. contains ESTs  
AU108280(E0721),D48017(S13927).

CAB51480.1 Y14600 *Sorghum bicolor*  
putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

AAC61805.1 U28007 *Lycopersicon esculentum*  
serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.

BAA87852.1 AP000816 *Oryza sativa*  
Similar to putative Ser/Thr protein kinase. (AC004218).

BAA92221.1 AP001278 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome II BAC F12L6 genomic sequence, putative  
protein kinase. (AC004218).

AAB09771.1 U67422 *Zea mays*  
CRINKLY4 precursor. cr4. receptor kinase homolog.

BAA90808.1 AP001168 *Oryza sativa*  
Similar to putative receptor-like protein kinase (AL035679).

AAC27894.1 AF023164 *Zea mays*  
leucine-rich repeat transmembrane protein kinase 1. ltk1.

AAB61708.1 U93048 *Daucus carota*  
somatic embryogenesis receptor-like kinase. SERK.

AAF91336.1	AF249317	Glycine max Ptil kinase-like protein. Ptila. protein kinase.
AAF91337.1	AF249318	Glycine max Ptil kinase-like protein. Ptilb. protein kinase.
AAG33377.1	AF290411	Oryza meyeriana serine/threonine protein kinase. R1.
AAC27895.1	AF023165	Zea mays leucine-rich repeat transmembrane protein kinase 2. Itk2.
AAK11566.1	AF318490	Lycopersicon hirsutum Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAF34428.1	AF172282	Oryza sativa receptor-like protein kinase. DUPR11.18.
AAF76306.1	AF220602	Lycopersicon pimpinellifolium Pto kinase.
AAB47423.1	U59315	Lycopersicon pimpinellifolium serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
AAC48914.1	U02271	Lycopersicon pimpinellifolium protein kinase.
AAK11567.1	AF318491	Lycopersicon hirsutum Pto-like protein kinase F. LhirPtoF.
AAB47421.1	U59316	Lycopersicon esculentum serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAF76313.1	AF220603	Lycopersicon esculentum Pto kinase. LescPth5.
AAF66615.1	AF142596	Nicotiana tabacum LRR receptor-like protein kinase.
BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA92953.1	AP001551	Oryza sativa Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).
SEQ ID NO: 479		
CAA42622.1	X60007	Nicotiana sylvestris nsGRP-2. putative glycine-rich protein of 19.7kDa.
SEQ ID NO: 480		
BAA83373.1	AP000391	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

BAA84787.1 AP000559 *Oryza sativa*  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

AAF91324.1 AF244890 *Glycine max*  
receptor-like protein kinase 3. RLK3. GmRLK3.

AAF91322.1 AF244888 *Glycine max*  
receptor-like protein kinase 1. RLK1. GmRLK1.

AAF91323.1 AF244889 *Glycine max*  
receptor-like protein kinase 2. RLK2. GmRLK2.

AAB36558.1 U77888 *Ipomoea nil*  
receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.

AAC36318.1 AF053127 *Malus x domestica*  
leucine-rich receptor-like protein kinase. LRPKm1.

AAF59906.1 AF197947 *Glycine max*  
receptor protein kinase-like protein. CLV1B.

BAB40094.1 AP003210 *Oryza sativa*  
putative receptor protein kinase. OSJNBA0010K01.7.

AAF59905.1 AF197946 *Glycine max*  
receptor protein kinase-like protein. CLV1A.

CAC20842.1 AJ250467 *Pinus sylvestris*  
receptor protein kinase. upk.

BAB03629.1 AP002522 *Oryza sativa*  
putative protein kinase Xa21. P0009G03.30.

BAB03621.1 AP002522 *Oryza sativa*  
putative protein kinase Xa21. P0009G03.21.

BAB03631.1 AP002522 *Oryza sativa*  
putative protein kinase Xa21. P0009G03.32.

AAB82755.1 U72725 *Oryza longistaminata*  
receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.

AAF34426.1 AF172282 *Oryza sativa*  
leucine rich repeat containing protein kinase. DUPR11.16.

AAK27806.1 AC022457 *Oryza sativa*  
putative protein kinase. OSJNBA0006L06.21.

CAA61510.1 X89226 *Oryza sativa*  
leucine-rich repeat/receptor protein kinase. lrk2.

AAC49123.1 U37133 *Oryza sativa*  
receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

AAC80225.1 U72723 *Oryza longistaminata*  
receptor kinase-like protein. Xa21. disease resistance gene.

AAK27817.1 AC022457 *Oryza sativa*  
putative protein kinase. OSJNBA0006L06.16.

BAA82393.1 AP000367 *Oryza sativa*

EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).

BAB03627.1 AP002522 *Oryza sativa*

putative protein kinase Xa21. P0009G03.27.

AAB82756.1 U72724 *Oryza sativa*

receptor kinase-like protein. Xa21 gene family member E.

AAG52992.1 U77888 *Ipomoea nil*

receptor-like protein kinase INRPK1a. inrpk1.

BAA88636.1 AB029327 *Nicotiana tabacum*

elicitor-inducible LRR receptor-like protein EILP. EILP.

AAB82753.1 U72726 *Oryza longistaminata*

receptor kinase-like protein. Xa21 gene family member D.

AAG52994.1 U77888 *Ipomoea nil*

receptor-like protein kinase INRPK1c. inrpk1.

CAB51480.1 Y14600 *Sorghum bicolor*

putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

AAK21965.1 AY028699 *Brassica napus*

receptor protein kinase PERK1.

SEQ ID NO: 481

CAB43505.1 AJ239051 *Cicer arietinum*

cytochrome P450. cyp81E2.

BAA22422.1 AB001379 *Glycyrrhiza echinata*

cytochrome P450. CYP81E1.

BAA93634.1 AB025016 *Lotus japonicus*

cytochrome P450.

BAA74465.1 AB022732 *Glycyrrhiza echinata*

cytochrome P450. CYP Ge-31.

CAB41490.1 AJ238439 *Cicer arietinum*

cytochrome P450 monooxygenase. cyp81E3v2.

CAA10067.1 AJ012581 *Cicer arietinum*

cytochrome P450. cyp81E3.

CAA04117.1 AJ000478 *Helianthus tuberosus*

fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-race).

CAA04116.1 AJ000477 *Helianthus tuberosus*

fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

AAK38080.1 AF321856 *Lolium rigidum*

putative cytochrome P450.

AAK38079.1 AF321855 *Lolium rigidum*

putative cytochrome P450.

AAK38081.1 AF321857 *Lolium rigidum*

putative cytochrome P450.

AAG09208.1 AF175278 *Pisum sativum*  
wound-inducible P450 hydroxylase. CYP82A1.

CAA71876.1 Y10982 *Glycine max*  
putative cytochrome P450.

AAC49188.2 U29333 *Pisum sativum*  
cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.

CAA65580.1 X96784 *Nicotiana tabacum*  
cytochrome P450. hsr515.

CAA71515.1 Y10491 *Glycine max*  
putative cytochrome P450.

BAA92894.1 AB006790 *Petunia x hybrida*  
cytochrome P450. IMT-2.

AAG44132.1 AF218296 *Pisum sativum*  
cytochrome P450. P450 isolog.

CAA64635.1 X95342 *Nicotiana tabacum*  
cytochrome P450. hsr515. hypersensitivity-related gene.

AAD56282.1 AF155332 *Petunia x hybrida*  
flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

AAC34853.1 AF082028 *Hemerocallis* hybrid cultivar  
putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3.  
mRNA accumulates in senescing petals.

BAA12159.1 D83968 *Glycine max*  
Cytochrome P-450 (CYP93A1).

AAA32913.1 M32885 *Persea americana*  
cytochrome P-450LXXIA1 (cyp71A1).

CAA70575.1 Y09423 *Nepeta racemosa*  
cytochrome P450. CYP71A5.

AAG34695.1 AF313492 *Matthiola incana*  
putative cytochrome P450.

CAA71877.1 Y10983 *Glycine max*  
putative cytochrome P450.

CAA71516.1 Y10492 *Glycine max*  
putative cytochrome P450.

AAB94587.1 AF022458 *Glycine max*  
CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

AAC39454.1 AF014802 *Eschscholzia californica*  
(S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent  
monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to  
wound-inducible CYP82A1 of *Pisum sativum* GenBank Accession Number U29333.

CAA70576.1 Y09424 *Nepeta racemosa*  
cytochrome P450. CYP71A6.

AAB94590.1 AF022461 *Glycine max*  
CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.

BAB40323.1 AB037244 *Asparagus officinalis*  
cytochrome P450. ASPI-1.

BAB40324.1 AB037245 *Asparagus officinalis*  
cytochrome P450. ASPI-2.

AAB61965.1 U48435 *Solanum chacoense*  
putative cytochrome P450.

AAA19701.1 L24438 *Thlaspi arvense*  
cytochrome P450.

BAA84071.1 AB028151 *Antirrhinum majus*  
flavone synthase II. cytochrome P450. AFNS2.

BAA13076.1 D86351 *Glycine max*  
cytochrome P-450 (CYP93A2).

AAD38930.1 AF135485 *Glycine max*  
cytochrome P450 monooxygenaseCYP93D1. CYP93E1.

AAC32274.1 AF081575 *Petunia x hybrida*  
flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.

SEQ ID NO: 487

BAA96181.1 AP002093 *Oryza sativa*

EST AU056651(S20760) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC F19I3; putative amino acid transporter (AC004238).

BAA96139.1 AP002092 *Oryza sativa*

EST AU056651(S20760) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC F19I3; putative amino acid transporter (AC004238).

SEQ ID NO: 495

AAB71528.1 U94784 *Helianthus annuus*  
ATPase. unconventional myosin. hamy4. Hamyo4.

AAB71529.1 U94785 *Helianthus annuus*  
ATPase. unconventional myosin. hamy5. Hamyo5.

AAB71527.1 U94782 *Helianthus annuus*  
ATPase. unconventional myosin. hamy2. Hamyo2.

AAD17931.2 AF104924 *Zea mays*  
unconventional myosin heavy chain. MYO1. ATPase; similar to myosin class XI.

AAC27525.1 AF077352 *Chlamydomonas reinhardtii*  
myosin heavy chain. MYO1. class XI.

AAK21311.1 AF338254 *Petroselinum crispum*  
myosin subfamily XI heavy chain. PCM3.

BAA87057.1 AB034154 *Chara corallina*  
unconventional myosin heavy chain. ccm.

BAB03273.1 AB007459 *Chara corallina*  
cytoplasmic streeming. myosin. ccm1. CCM1.

AAF43440.1 AF233886 *Vallisneria gigantea*  
unconventional myosin XI. VMYO1.

AAB53062.1 U94398 *Acetabularia cliftonii*  
myosin. myo2.

AAD34597.1 AF147739 *Zea mays*  
myosin XI. M2. unconventional myosin.

AAB53061.1 U94397 *Acetabularia cliftonii*  
myosin. myo1.

AAD31926.1 AF147738 *Zea mays*  
myosin VIII ZMM3. zmm3. unconventional myosin.

AAB71526.1 U94781 *Helianthus annuus*  
unconventional myosin. hamy1. homologous to ATM1.

AAG49341.1 AF319457 *Petroselinum crispum*  
myosin subfamily VIII heavy chain.

AAB93521.1 U94783 *Helianthus annuus*  
unconventional myosin. hamy3. Hamyo3; similar to class VIII myosin.

CAA47476.1 X67102 *Anemia phyllitidis*  
myosin heavy chain. myo15.

CAA47477.1 X67103 *Anemia phyllitidis*  
myosin heavy chain. myo22.

AAF43441.1 AF233887 *Vallisneria gigantea*  
unconventional myosin VIII. VMYO2.

AAG13633.1 AC078840 *Oryza sativa*  
putative myosin. OSJNBb0073N24.16.

AAA92120.1 U48785 *Vigna mungo*  
plant myosin MBM1. mbm1. head coding region.

SEQ ID NO: 496

AAA34138.1 M96324 *Lycopersicon esculentum*  
The calcium ATPase is a calcium ion pump. Ca2+-ATPase. LCA1.

AAD11618.1 AF050496 *Lycopersicon esculentum*  
Ca2+-ATPase. LCA1B; alternative transcript.

AAD11617.1 AF050495 *Lycopersicon esculentum*  
Ca2+-ATPase. LCA1A; alternative transcript.

BAA90510.2 AP001111 *Oryza sativa*  
rice EST AU030811, similar to rice Ca+2-ATPase (U82966).

CAA63790.1 X93592 *Dunaliella bioculata*  
P-type ATPase. ca1. calcium pumping; CA1.

AAB58910.1 U82966 *Oryza sativa*  
Ca2+-ATPase.

AAF73985.1 AF096871 *Zea mays*  
calcium pump. calcium ATPase. cap1.

AAG28436.1	AF195029	Glycine max plasma membrane Ca <sup>2+</sup> -ATPase. SCA2.
AAG28435.1	AF195028	Glycine max plasma membrane Ca <sup>2+</sup> -ATPase. SCA1.
CAA68234.1	X99972	Brassica oleracea calmodulin-stimulated calcium-ATPase.
AAD31896.1	AF145478	Mesembryanthemum crystallinum calcium ATPase.
CAB85494.1	AJ132891	Medicago truncatula proton pump. H <sup>+</sup> -ATPase. ha1.
CAB85495.1	AJ132892	Medicago truncatula proton pump. H <sup>+</sup> -ATPase. ha1.
CAB69824.1	AJ271439	Prunus persica plasma membrane H <sup>+</sup> ATPase. PPA1.
CAA52107.1	X73901	Dunaliella bioculata plasma membrane ATPase. pma1.
AAD46188.1	AF156691	Nicotiana plumbaginifolia plasma membrane proton ATPase. pma9.
BAA01058.1	D10207	Oryza sativa H-ATPase. OSA1.
AAA34094.1	M80489	Nicotiana plumbaginifolia plasma membrane H <sup>+</sup> ATPase. pma1.
AAA34098.1	M80490	Nicotiana plumbaginifolia plasma membrane H <sup>+</sup> ATPase. pma3.
AAA34173.1	M60166	Lycopersicon esculentum H <sup>+</sup> -ATPase. LHA1.
CAA54046.1	X76536	Solanum tuberosum H(+) -transporting ATPase. PHA1.
AAD55399.1	AF179442	Lycopersicon esculentum plasma membrane H <sup>+</sup> -ATPase isoform LHA2. LHA2.
AAB49042.1	U54690	Dunaliella acidophila plasma membrane proton ATPase. dha1. DaDHA1; proton pump.
AAF98344.1	AF275745	Lycopersicon esculentum plasma membrane H <sup>+</sup> -ATPase. LHA2. P-type ion pump.
BAA08134.1	D45189	Zostera marina plasma membrane H <sup>+</sup> -ATPase. zha1.
AAA34052.1	M27888	Nicotiana plumbaginifolia H <sup>+</sup> -translocating ATPase.
CAA59800.1	X85805	Zea mays H(+) -transporting ATPase. MHA-2.
AAB17186.1	U72148	Lycopersicon esculentum plasma membrane H <sup>+</sup> -ATPase. LHA4. plasma membrane proton pumping ATPase.

CAA54045.1	X76535	Solanum tuberosum H(+) -transporting ATPase. PHA2.
CAB69823.1	AJ271438	Prunus persica plasma membrane H <sup>+</sup> ATPase. PPA2.
BAA06629.1	D31843	Oryza sativa plasma membrane H <sup>+</sup> -ATPase. OSA2.
CAC29435.1	AJ310523	Vicia faba P-type H <sup>+</sup> -ATPase. vha4. predominantly expressed in flowers.
CAC29436.1	AJ310524	Vicia faba P-type H <sup>+</sup> -ATPase. ha5. predominantly expressed in guard cells and flowers.
CAA59799.1	X85804	Phaseolus vulgaris H(+) -transporting ATPase. BHA-1.
AAD46186.1	AF156679	Nicotiana plumbaginifolia plasma membrane proton ATPase. pma6.
AAB84202.2	AF029256	Kosteletzky virginica plasma membrane proton ATPase. ATP1.
AAD46187.1	AF156683	Nicotiana plumbaginifolia plasma membrane proton ATPase. pma8.
AAB60276.1	U09989	Zea mays H(+) -transporting ATPase. Mhal.
AAB41898.1	U84891	Mesembryanthemum crystallinum plasma membrane proton pump. H <sup>+</sup> -transporting ATPase. PMA.
AAB35314.2	S79323	Vicia faba plasma membrane H(+) -ATPase precursor. plasma membrane H(+) -ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
AAK31799.1	AY029190	Lilium longiflorum plasma membrane H <sup>+</sup> ATPase. LILHA1.
CAA47275.1	X66737	Nicotiana plumbaginifolia plasma membrane H <sup>+</sup> -ATPase. pma4.
BAA37150.1	AB022442	Vicia faba p-type H <sup>+</sup> -ATPase. VHA2.
AAG01028.1	AF289025	Cucumis sativus plasma membrane H <sup>+</sup> -ATPase.
AAA81348.1	U38965	Vicia faba p-type H <sup>+</sup> -ATPase. VHA2.
AAK32118.1	AF308816	Hordeum vulgare plasmalemma H <sup>+</sup> -ATPase 1.
AAF97591.1	AF263917	Lycopersicon esculentum plasma membrane proton ATPase. LHA8.
AAK32119.1	AF308817	Hordeum vulgare plasmalemma H <sup>+</sup> -ATPase 2.

AAA20601.1 U08985 Zea mays  
plasma-membrane H<sup>+</sup> ATPase. Zmpma1.

SEQ ID NO: 497

AAB41742.1 U82559 *Lycopersicon esculentum*

aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

AAB41741.1 U82558 *Lycopersicon esculentum*

aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

SEQ ID NO: 498

CAA73134.1 Y12531 *Brassica oleracea*  
serine/threonine kinase. BRLK.

AAB93834.1 U82481 Zea mays

KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

CAA67145.1 X98520 *Brassica oleracea*  
receptor-like kinase. SFR2.

CAA74661.1 Y14285 *Brassica oleracea*

SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

CAA73133.1 Y12530 *Brassica oleracea*  
serine /threonine kinase. ARLK.

AAA62232.1 U00443 *Brassica napus*

S-receptor kinase. protein contains an immunoglobulin-like domain.

CAB89179.1 AJ245479 *Brassica napus* subsp. napus  
ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 *Brassica napus*  
serine/threonine kinase receptor.

BAA92836.1 AB032473 *Brassica oleracea*  
S18 S-locus receptor kinase. SRK18.

BAA23676.1 AB000970 *Brassica rapa*  
receptor kinase 1. BcRK1.

AAC23542.1 U20948 *Ipomoea trifida*  
receptor protein kinase. IRK1.

AAA33000.1 M76647 *Brassica oleracea*  
receptor protein kinase. SKR6.

BAA21132.1 D88193 *Brassica rapa*  
S-receptor kinase. SRK9 (B.c.).

BAA06285.1 D30049 *Brassica rapa*  
S-receptor kinase SRK9.

CAB41879.1	Y18260	Brassica oleracea
SRK15 protein. SRK15. receptor-like kinase.		
BAA07577.2	D38564	Brassica rapa
receptor protein kinase SRK12.		
CAA74662.1	Y14286	Brassica oleracea
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.		
BAB21001.1	AB054061	Brassica rapa
S locus receptor kinase. SRK22.		
BAA92837.1	AB032474	Brassica oleracea
S60 S-locus receptor kinase. SRK60.		
CAB41878.1	Y18259	Brassica oleracea
SRK5 protein. SRK5. receptor-like kinase.		
CAA79355.1	Z18921	Brassica oleracea
S-receptor kinase-like protein.		
BAA07576.1	D38563	Brassica rapa
receptor protein kinase SRK8.		
AAF34428.1	AF172282	Oryza sativa
receptor-like protein kinase. DUPR11.18.		
AAD21872.1	AF078082	Phaseolus vulgaris
receptor-like protein kinase homolog RK20-1.		
AAD52097.1	AF088885	Nicotiana tabacum
receptor-like kinase CHRK1. Chrk1.		
BAA94516.1	AP001800	Oryza sativa
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).		
BAB07906.1	AP002835	Oryza sativa
putative S-receptor kinase. P0417G05.14.		
BAA94517.1	AP001800	Oryza sativa
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).		
BAB07905.1	AP002835	Oryza sativa
putative S-receptor kinase. P0417G05.13.		
AAA33915.1	L27821	Oryza sativa
receptor type serine/threonine kinase. protein kinase.		
BAB18292.1	AP002860	Oryza sativa
putative receptor-like protein kinase. P0409B08.19.		
BAA94529.2	AP001800	Oryza sativa
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).		
SEQ ID NO: 499		
AAC36318.1	AF053127	Malus x domestica
leucine-rich receptor-like protein kinase. LRPKm1.		
AAF91324.1	AF244890	Glycine max
receptor-like protein kinase 3. RLK3. GmRLK3.		

AAF91323.1 AF244889 Glycine max  
receptor-like protein kinase 2. RLK2. GmRLK2.

CAA61510.1 X89226 Oryza sativa  
leucine-rich repeat/receptor protein kinase. lrk2.

AAF59906.1 AF197947 Glycine max  
receptor protein kinase-like protein. CLV1B.

AAF59905.1 AF197946 Glycine max  
receptor protein kinase-like protein. CLV1A.

AAF91322.1 AF244888 Glycine max  
receptor-like protein kinase 1. RLK1. GmRLK1.

BAB40094.1 AP003210 Oryza sativa  
putative receptor protein kinase. OSJNBa0010K01.7.

CAC20842.1 AJ250467 Pinus sylvestris  
receptor protein kinase. upk.

AAB36558.1 U77888 Ipomoea nil  
receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.

BAA83373.1 AP000391 Oryza sativa  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

BAA84787.1 AP000559 Oryza sativa  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

AAK27806.1 AC022457 Oryza sativa  
putative protein kinase. OSJNBa0006L06.21.

AAF34426.1 AF172282 Oryza sativa  
leucine rich repeat containing protein kinase. DUPR11.16.

BAB03627.1 AP002522 Oryza sativa  
putative protein kinase Xa21. P0009G03.27.

BAB03631.1 AP002522 Oryza sativa  
putative protein kinase Xa21. P0009G03.32.

AAK27817.1 AC022457 Oryza sativa  
putative protein kinase. OSJNBa0006L06.16.

BAB03621.1 AP002522 Oryza sativa  
putative protein kinase Xa21. P0009G03.21.

BAB03629.1 AP002522 Oryza sativa  
putative protein kinase Xa21. P0009G03.30.

AAC80225.1 U72723 Oryza longistaminata  
receptor kinase-like protein. Xa21. disease resistance gene.

AAC49123.1 U37133 Oryza sativa  
receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

BAA82393.1 AP000367 Oryza sativa  
EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).

AAB82755.1 U72725 Oryza longistaminata  
receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.

AAG52992.1 U77888 Ipomoea nil  
receptor-like protein kinase INRPK1a. inrpk1.

AAB82756.1 U72724 Oryza sativa  
receptor kinase-like protein. Xa21 gene family member E.

AAB82753.1 U72726 Oryza longistaminata  
receptor kinase-like protein. Xa21 gene family member D.

CAB51480.1 Y14600 Sorghum bicolor  
putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

BAA88636.1 AB029327 Nicotiana tabacum  
elicitor-inducible LRR receptor-like protein EILP. EILP.

AAG52994.1 U77888 Ipomoea nil  
receptor-like protein kinase INRPK1c. inrpk1.

BAA94519.1 AP001800 Oryza sativa  
ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene.  
Similar to Arabidopsis thaliana chromosome 4, BAC F9D16; putative receptor kinase (AL035394).

BAB07903.1 AP002835 Oryza sativa  
putative receptor kinase. P0417G05.10. contains ESTs  
AU032341(R3918),AU071016(R10613).

BAA87853.1 AP000816 Oryza sativa  
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

AAD38286.1 AC007789 Oryza sativa  
putative protein kinase. OSJNBa0049B20.13.

BAB40081.1 AP003074 Oryza sativa  
putative receptor protein kinase. OSJNBa0004G10.30.

BAB18321.1 AP002865 Oryza sativa  
putative receptor protein kinase. P0034C11.11.

SEQ ID NO: 500

BAB40094.1 AP003210 Oryza sativa  
putative receptor protein kinase. OSJNBa0010K01.7.

AAC36318.1 AF053127 Malus x domestica  
leucine-rich receptor-like protein kinase. LRPKm1.

AAF59906.1 AF197947 Glycine max  
receptor protein kinase-like protein. CLV1B.

AAF59905.1 AF197946 Glycine max  
receptor protein kinase-like protein. CLV1A.

AAF91323.1 AF244889 Glycine max  
receptor-like protein kinase 2. RLK2. GmRLK2.

AAF91322.1	AF244888	Glycine max receptor-like protein kinase 1. RLK1. GmRLK1.
AAF91324.1	AF244890	Glycine max receptor-like protein kinase 3. RLK3. GmRLK3.
CAA61510.1	X89226	Oryza sativa leucine-rich repeat/receptor protein kinase. lrk2.
CAC20842.1	AJ250467	Pinus sylvestris receptor protein kinase. upk.
BAA84787.1	AP000559	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA83373.1	AP000391	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
AAK27806.1	AC022457	Oryza sativa putative protein kinase. OSJNBa0006L06.21.
AAB36558.1	U77888	Ipomoea nil receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
BAB03627.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.27.
BAB03629.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.30.
BAB03631.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.32.
BAB03621.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.21.
AAK27817.1	AC022457	Oryza sativa putative protein kinase. OSJNBa0006L06.16.
AAF34426.1	AF172282	Oryza sativa leucine rich repeat containing protein kinase. DUPR11.16.
AAB82755.1	U72725	Oryza longistaminata receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
AAC80225.1	U72723	Oryza longistaminata receptor kinase-like protein. Xa21. disease resistance gene.
AAC49123.1	U37133	Oryza sativa receptor kinase-like protein. Xa21. Xa21 disease resistance gene.
BAA82393.1	AP000367	Oryza sativa EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).
AAB82756.1	U72724	Oryza sativa receptor kinase-like protein. Xa21 gene family member E.

BAA88636.1	AB029327	Nicotiana tabacum elicitor-inducible LRR receptor-like protein EILP. EILP.
AAG52992.1	U77888	Ipomoea nil receptor-like protein kinase INRPK1a. inrpk1.
AAB82753.1	U72726	Oryza longistaminata receptor kinase-like protein. Xa21 gene family member D.
CAB51480.1	Y14600	Sorghum bicolor putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
AAB61708.1	U93048	Daucus carota somatic embryogenesis receptor-like kinase. SERK.
		SEQ ID NO: 501
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
BAA92836.1	AB032473	Brassica oleracea S18 S-locus receptor kinase. SRK18.
CAB41878.1	Y18259	Brassica oleracea SRK5 protein. SRK5. receptor-like kinase.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
CAB41879.1	Y18260	Brassica oleracea SRK15 protein. SRK15. receptor-like kinase.
AAA33000.1	M76647	Brassica oleracea receptor protein kinase. SKR6.
AAA33008.1	M97667	Brassica napus serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus ser /thr kinase. S-locus receptor kinase. srk.

CAA74662.1	Y14286	Brassica oleracea
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.		
BAA06285.1	D30049	Brassica rapa
S-receptor kinase SRK9.		
BAA21132.1	D88193	Brassica rapa
S-receptor kinase. SRK9 (B.c).		
BAA07577.2	D38564	Brassica rapa
receptor protein kinase SRK12.		
CAA79355.1	Z18921	Brassica oleracea
S-receptor kinase-like protein.		
BAA07576.1	D38563	Brassica rapa
receptor protein kinase SRK8.		
BAB21001.1	AB054061	Brassica rapa
S locus receptor kinase. SRK22.		
BAA92837.1	AB032474	Brassica oleracea
S60 S-locus receptor kinase. SRK60.		
AAD21872.1	AF078082	Phaseolus vulgaris
receptor-like protein kinase homolog RK20-1.		
AAF34428.1	AF172282	Oryza sativa
receptor-like protein kinase. DUPR11.18.		
AAD52097.1	AF088885	Nicotiana tabacum
receptor-like kinase CHRK1. Chrk1.		
BAB07906.1	AP002835	Oryza sativa
putative S-receptor kinase. P0417G05.14.		
BAA94516.1	AP001800	Oryza sativa
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).		
BAB18292.1	AP002860	Oryza sativa
putative receptor-like protein kinase. P0409B08.19.		
BAB07904.1	AP002835	Oryza sativa
putative S-receptor kinase. P0417G05.12.		
BAA94518.1	AP001800	Oryza sativa
Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).		

SEQ ID NO: 502

AAC78596.1	AF053998	Lycopersicon esculentum
Hcr2-5D. Hcr2-5D. similar to Lycopersicon pimpinellifolium disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.		
AAC78591.1	AF053993	Lycopersicon esculentum
disease resistance protein. Cf-5.		
AAC78593.1	AF053995	Lycopersicon esculentum
Hcr2-0B. Hcr2-0B. similar to Lycopersicon pimpinellifolium disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.		

AAC78592.1 AF053994 *Lycopersicon esculentum*  
Hcr2-0A. Hcr2-0A. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2  
encoded by the sequence presented in GenBank Accession Number U42445.

AAC78594.1 AF053996 *Lycopersicon pimpinellifolium*  
Hcr2-2A. Hcr2-2A. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2  
encoded by the sequence presented in GenBank Accession Number U42445.

CAA05274.1 AJ002236 *Lycopersicon pimpinellifolium*  
resistance gene. Cf-9. Cf-9.

AAA65235.1 U15936 *Lycopersicon pimpinellifolium*  
Cf-9 precursor. Cf-9. this is the ninth resistance gene to disease caused by *Cladosporium*  
fulvum to be isolated.

CAA05276.1 AJ002236 *Lycopersicon pimpinellifolium*  
resistance gene. Hcr9-9E. Hcr9-9E.

AAC78595.1 AF053997 *Lycopersicon esculentum*  
Hcr2-5B. Hcr2-5B. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2  
encoded by the sequence presented in GenBank Accession Number U42445.

CAA05268.1 AJ002235 *Lycopersicon hirsutum*  
Resistance gene. Cf-4. Cf-4.

CAA05279.1 AJ002237 *Lycopersicon esculentum*  
Hcr9-0. Hcr9-0. homologue of *Cladosporium fulvum* disease resistance gene Cf-9.

BAB08215.1 AP002539 *Oryza sativa*  
Similar to *Lycopersicon esculentum* disease resistance protein (AF053993).

BAA96776.1 AP002521 *Oryza sativa*  
Similar to *Lycopersicon esculentum* disease resistance protein (AF053993).

AAG21897.1 AC026815 *Oryza sativa*  
putative disease resistance protein (3' partial). OSJNBa0079L16.21.

AAD50430.1 AF166121 *Hordeum vulgare*  
Cf2/Cf5 disease resistance protein homolog. Big1. leucine rich repeat protein.

AAG21917.1 AC026815 *Oryza sativa*  
putative disease resistance protein. OSJNBa0079L16.5.

CAB55409.1 AL117265 *Oryza sativa*  
zhb0001.1. Incomplete at 5'end,Similar to disease resistance protein; Method: conceptual  
translation with partial peptide sequencing.

AAG21909.1 AC026815 *Oryza sativa*  
putative disease resistance protein. OSJNBa0079L16.3.

AAC80225.1 U72723 *Oryza longistaminata*  
receptor kinase-like protein. Xa21. disease resistance gene.

AAC49123.1 U37133 *Oryza sativa*  
receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

SEQ ID NO: 503

CAA05276.1 AJ002236 *Lycopersicon pimpinellifolium*  
resistance gene. Hcr9-9E. Hcr9-9E.

AAC78592.1	AF053994	Lycopersicon esculentum
Hcr2-0A. Hcr2-0A. similar to Lycopersicon pimpinellifolium disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.		
CAA05274.1	AJ002236	Lycopersicon pimpinellifolium
resistance gene. Cf-9. Cf-9.		
AAA65235.1	U15936	Lycopersicon pimpinellifolium
Cf-9 precursor. Cf-9. this is the ninth resistance gene to disease caused by Cladosporium fulvum to be isolated.		
AAC78594.1	AF053996	Lycopersicon pimpinellifolium
Hcr2-2A. Hcr2-2A. similar to Lycopersicon pimpinellifolium disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.		
CAA05279.1	AJ002237	Lycopersicon esculentum
Hcr9-0. Hcr9-0. homologue of Cladosporium fulvum disease resistance gene Cf-9.		
AAC78595.1	AF053997	Lycopersicon esculentum
Hcr2-5B. Hcr2-5B. similar to Lycopersicon pimpinellifolium disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.		
AAC78593.1	AF053995	Lycopersicon esculentum
Hcr2-0B. Hcr2-0B. similar to Lycopersicon pimpinellifolium disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.		
CAA05268.1	AJ002235	Lycopersicon hirsutum
Resistance gene. Cf-4. Cf-4.		
AAC78596.1	AF053998	Lycopersicon esculentum
Hcr2-5D. Hcr2-5D. similar to Lycopersicon pimpinellifolium disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.		
AAC78591.1	AF053993	Lycopersicon esculentum
disease resistance protein. Cf-5.		
BAA96776.1	AP002521	Oryza sativa
Similar to Lycopersicon esculentum disease resistance protein (AF053993).		
BAB08215.1	AP002539	Oryza sativa
Similar to Lycopersicon esculentum disease resistance protein (AF053993).		
CAB55409.1	AL117265	Oryza sativa
zhb0001.1. Incomplete at 5'end,Similar to disease resistance protein; Method: conceptual translation with partial peptide sequencing.		
AAD50430.1	AF166121	Hordeum vulgare
Cf2/Cf5 disease resistance protein homolog. Big1. leucine rich repeat protein.		
AAG21897.1	AC026815	Oryza sativa
putative disease resistance protein (3' partial). OSJNBa0079L16.21.		
AAB82755.1	U72725	Oryza longistaminata
receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.		
SEQ ID NO: 504		
AAF91324.1	AF244890	Glycine max
receptor-like protein kinase 3. RLK3. GmRLK3.		

BAA84787.1 AP000559 Oryza sativa  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

BAA83373.1 AP000391 Oryza sativa  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

AAF91322.1 AF244888 Glycine max  
receptor-like protein kinase 1. RLK1. GmRLK1.

AAF91323.1 AF244889 Glycine max  
receptor-like protein kinase 2. RLK2. GmRLK2.

CAC20842.1 AJ250467 Pinus sylvestris  
receptor protein kinase. upk.

AAK27806.1 AC022457 Oryza sativa  
putative protein kinase. OSJNBa0006L06.21.

AAB36558.1 U77888 Ipomoea nil  
receptor-like protein kinase INRPK1. inrpkl. leucine-rich repeat.

BAA82393.1 AP000367 Oryza sativa  
EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).

AAF59906.1 AF197947 Glycine max  
receptor protein kinase-like protein. CLV1B.

BAB03629.1 AP002522 Oryza sativa  
putative protein kinase Xa21. P0009G03.30.

BAB03627.1 AP002522 Oryza sativa  
putative protein kinase Xa21. P0009G03.27.

AAF59905.1 AF197946 Glycine max  
receptor protein kinase-like protein. CLV1A.

AAK27817.1 AC022457 Oryza sativa  
putative protein kinase. OSJNBa0006L06.16.

BAB03631.1 AP002522 Oryza sativa  
putative protein kinase Xa21. P0009G03.32.

BAB03621.1 AP002522 Oryza sativa  
putative protein kinase Xa21. P0009G03.21.

AAF34426.1 AF172282 Oryza sativa  
leucine rich repeat containing protein kinase. DUPR11.16.

AAF66615.1 AF142596 Nicotiana tabacum  
LRR receptor-like protein kinase.

AAB82755.1 U72725 Oryza longistaminata  
receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.

AAC49123.1 U37133 Oryza sativa  
receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

AAC80225.1	U72723	Oryza longistaminata receptor kinase-like protein. Xa21. disease resistance gene.
BAB19337.1	AP003044	Oryza sativa putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
BAA88636.1	AB029327	Nicotiana tabacum elicitor-inducible LRR receptor-like protein EILP. EILP.
CAB51480.1	Y14600	Sorghum bicolor putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB07903.1	AP002835	Oryza sativa putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).
BAA94519.1	AP001800	Oryza sativa ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> chromosome 4, BAC F9D16; putative receptor kinase (AL035394).
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
AAG59657.1	AC084319	Oryza sativa putative protein kinase. OSJNBa0004B24.20.
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAB82756.1	U72724	Oryza sativa receptor kinase-like protein. Xa21 gene family member E.
AAB82753.1	U72726	Oryza longistaminata receptor kinase-like protein. Xa21 gene family member D.
SEQ ID NO: 505		
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.

BAA23676.1 AB000970 Brassica rapa  
receptor kinase 1. BcRK1.

AAB93834.1 U82481 Zea mays  
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

CAA73133.1 Y12530 Brassica oleracea  
serine /threonine kinase. ARLK.

CAA67145.1 X98520 Brassica oleracea  
receptor-like kinase. SFR2.

CAB89179.1 AJ245479 Brassica napus subsp. napus  
ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 Brassica napus  
serine/threonine kinase receptor.

BAA21132.1 D88193 Brassica rapa  
S-receptor kinase. SRK9 (B.c.).

AAA62232.1 U00443 Brassica napus  
S-receptor kinase. protein contains an immunoglobulin-like domain.

BAA06285.1 D30049 Brassica rapa  
S-receptor kinase SRK9.

CAA74662.1 Y14286 Brassica oleracea  
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

AAA33000.1 M76647 Brassica oleracea  
receptor protein kinase. SKR6.

BAA07576.1 D38563 Brassica rapa  
receptor protein kinase SRK8.

BAA92836.1 AB032473 Brassica oleracea  
S18 S-locus receptor kinase. SRK18.

CAB41878.1 Y18259 Brassica oleracea  
SRK5 protein. SRK5. receptor-like kinase.

CAA79355.1 Z18921 Brassica oleracea  
S-receptor kinase-like protein.

CAB41879.1 Y18260 Brassica oleracea  
SRK15 protein. SRK15. receptor-like kinase.

BAB21001.1 AB054061 Brassica rapa  
S locus receptor kinase. SRK22.

BAA92837.1 AB032474 Brassica oleracea  
S60 S-locus receptor kinase. SRK60.

BAA07577.2 D38564 Brassica rapa  
receptor protein kinase SRK12.

AAD21872.1 AF078082 Phaseolus vulgaris  
receptor-like protein kinase homolog RK20-1.

BAA94517.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.13.
BAB07906.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.14.
BAA94516.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
AAD52097.1	AF088885	Nicotiana tabacum receptor-like kinase CHRK1. Chrk1.
BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
SEQ ID NO: 507		
AAA33509.1	M62985	Zea mays protein kinase. putative; putative.
CAA62476.1	X90990	Solanum tuberosum stpk1 protein kinase.
AAK31277.1	AC079890	Oryza sativa putative protein kinase. OSJNBb0089A17.15.
CAA66616.1	X97980	Solanum berthaultii protein kinase.
AAF66637.1	AF143505	Lycopersicon esculentum viroid symptom modulation protein. PKv. protein kinase; induced by viroid infection.
BAA96593.1	AP002481	Oryza sativa Similar to Solanum berthaultii protein kinase. (X97980).
AAB54117.1	U93559	Brassica rapa putative serine/threonine protein kinase. Bcpk1.
AAB88817.1	AF033263	Zea mays signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat NPH1 proteins.
AAC05084.1	AF033097	Avena sativa NPH1-2. NPH1-2. putative serine/threonine protein kinase.
CAA82994.1	Z30333	Mesembryanthemum crystallinum protein kinase.
AAC05083.1	AF033096	Avena sativa NPH1-1. NPH1-1. putative serine/threonine protein kinase.
CAA82992.1	Z30331	Mesembryanthemum crystallinum Protein Kinase.
CAA82993.1	Z30332	Spinacia oleracea protein kinase.
AAA50304.1	M92989	Pisum sativum protein kinase. PK5. homologue.

AAB71418.1 U11553 *Pisum sativum*  
PsPK3. putative protein kinase.

BAA93704.1 AB032564 *Cucumis sativus*  
cucumber protein kinase CsPK3. CsPK3. putative.

BAA36192.1 AB012082 *Adiantum capillus-veneris*  
PHY3. PHY3. Ser/Thr protein kinase; chimeric structure of red/far-red light photoreceptive region (phytochrome) and putative blue light photoreceptor in phototropism of hypocotyl (NPH1).

AAK18843.1 AC082645 *Oryza sativa*  
putative protein kinase. OSJNBB0033N16.3.

CAB82852.1 Z30329 *Mesembryanthemum crystallinum*  
protein kinase MK6.

CAA50374.1 X71057 *Nicotiana tabacum*  
protein kinase. PKTL7.

AAK13156.1 AC078829 *Oryza sativa*  
putative protein kinase. OSJNBB0026O12.14.

BAB03409.1 AP002816 *Oryza sativa*  
Similar to *Spinacia oleracea* protein kinase (S42867).

CAA82991.1 Z30330 *Spinacia oleracea*  
protein kinase.

AAD50584.1 AF089097 *Salvia columbariae*  
protein kinase 1. PK1.

AAB93860.1 U89679 *Lycopersicon esculentum*  
protein kinase. LePK2. contains catalytic domain.

AAD50585.1 AF089099 *Salvia columbariae*  
protein kinase 3. PK3.

AAD50586.1 AF089100 *Salvia columbariae*  
protein kinase 4. PK4.

AAB93859.1 U89678 *Lycopersicon esculentum*  
protein kinase. LePK1. contains catalytic domain.

AAA50772.1 M69030 *Pisum sativum*  
protein serine/threonine kinase. PsPK1. putative; putative.

AAB93861.1 U89680 *Lycopersicon esculentum*  
protein kinase. LePK3. contains catalytic domain.

AAD50587.1 AF089101 *Salvia columbariae*  
protein kinase 5. PK5.

AAD50588.1 AF089102 *Salvia columbariae*  
protein kinase 6. PK6.

CAA56313.1 X79992 *Avena sativa*  
putative pp70 ribosomal protein S6 kinase. Aspk11.

AAD50589.1 AF089103 *Salvia columbariae*  
protein kinase 7. PK7.

CAB89082.1	AJ277534	Asparagus officinalis S6 ribosomal protein kinase. pk1. putative.
AAB93862.1	U89681	Lycopersicon esculentum protein kinase. LePK4. contains catalytic domain.
BAA92972.1	AP001551	Oryza sativa ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).
BAB12687.1	AP002746	Oryza sativa putative protein kinase. P0671B11.2. contains ESTs C22394(C30013),C22393(C30013).
		SEQ ID NO: 508
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
CAA74662.1	Y14286	Brassica oleracea SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
AAA33008.1	M97667	Brassica napus serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus ser /thr kinase. S-locus receptor kinase. srk.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
CAB41878.1	Y18259	Brassica oleracea SRK5 protein. SRK5. receptor-like kinase.
AAA33000.1	M76647	Brassica oleracea receptor protein kinase. SKR6.
BAA92837.1	AB032474	Brassica oleracea S60 S-locus receptor kinase. SRK60.
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c.).
BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
BAA92836.1	AB032473	Brassica oleracea S18 S-locus receptor kinase. SRK18.

BAB21001.1 AB054061 *Brassica rapa*  
S locus receptor kinase. SRK22.

BAA07576.1 D38563 *Brassica rapa*  
receptor protein kinase SRK8.

BAA07577.2 D38564 *Brassica rapa*  
receptor protein kinase SRK12.

CAA73134.1 Y12531 *Brassica oleracea*  
serine/threonine kinase. BRLK.

AAB93834.1 U82481 *Zea mays*  
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

AAC23542.1 U20948 *Ipomoea trifida*  
receptor protein kinase. IRK1.

CAB41879.1 Y18260 *Brassica oleracea*  
SRK15 protein. SRK15. receptor-like kinase.

AAD52097.1 AF088885 *Nicotiana tabacum*  
receptor-like kinase CHRK1. Chrk1.

AAD21872.1 AF078082 *Phaseolus vulgaris*  
receptor-like protein kinase homolog RK20-1.

BAB18292.1 AP002860 *Oryza sativa*  
putative receptor-like protein kinase. P0409B08.19.

AAK02023.1 AC074283 *Oryza sativa*  
Putative protein kinase-like. OSJNBA0087H07.5.

CAA79324.1 Z18884 *Brassica oleracea*  
S-receptor kinase related protein.

BAB21240.1 AP002953 *Oryza sativa*  
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

CAB51836.1 AJ243961 *Oryza sativa*  
Putitive Ser/Thr protein kinase. I1332.7.

AAK21965.1 AY028699 *Brassica napus*  
receptor protein kinase PERK1.

BAB39873.1 AP002882 *Oryza sativa*  
putative protein kinase. P0439B06.8. contains ESTs  
AU056701(S20808),AU056702(S20808).

BAA94509.1 AB041503 *Populus nigra*  
protein kinase 1. PnPK1.

AAK00425.1 AC069324 *Oryza sativa*  
Putative protein kinase. OSJNBA0071K19.11.

BAA94510.1 AB041504 *Populus nigra*  
protein kinase 2. PnPK2.

BAA92953.1 AP001551 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).

BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
		SEQ ID NO: 510
AAG30254.1	AF307333	Hordeum vulgare putative nematode-resistance protein. Hs1. similar to Beta procumbens Hs1pro protein.
AAB48305.1	U79733	Beta procumbens nematode resistance. Hs1pro-1.
		SEQ ID NO: 513
BAA14144.1	D90116	Armoracia rusticana peroxidase isozyme.
BAA14143.1	D90115	Armoracia rusticana peroxidase isozyme.
BAA11853.1	D83225	Populus nigra peroxidase.
CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA11852.1	D83224	Populus nigra peroxidase.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
BAA06335.1	D30653	Populus kitakamiensis peroxidase.
AAB47602.1	L07554	Linum usitatissimum peroxidase. FLXPER1.
AAC98519.1	AF007211	Glycine max peroxidase precursor. GMIPER1. pathogen-induced.
AAD37427.1	AF149277	Phaseolus vulgaris peroxidase 1 precursor. FBP1. secretory peroxidase.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
AAB97734.1	AF014502	Glycine max seed coat peroxidase precursor. Ep. H <sub>2</sub> O <sub>2</sub> oxidoreductase; class III plant peroxidase.

CAB94692.1 AJ242742 *Ipomoea batatas*  
Removal of H<sub>2</sub>O<sub>2</sub>, oxidation of toxic reductants, defence response toward wounding.  
peroxidase. pod.

CAA62227.1 X90694 *Medicago sativa*  
peroxidase1C. prx1C.

CAA62226.1 X90693 *Medicago sativa*  
peroxidase1B. prx1B.

AAD37430.1 AF149280 *Phaseolus vulgaris*  
peroxidase 5 precursor. FBP5. secretory peroxidase.

CAA62225.1 X90692 *Medicago sativa*  
peroxidase1A. prx1A.

AAB41811.1 L36157 *Medicago sativa*  
peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.

AAB41810.1 L36156 *Medicago sativa*  
peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.

BAA01877.1 D11102 *Populus kitakamiensis*  
peroxidase. prxA1.

CAB67121.1 Y19023 *Lycopersicon esculentum*  
peroxidase. cevi-1.

CAA50597.1 X71593 *Lycopersicon esculentum*  
peroxidase. CEVI-1.

BAA01992.1 D11396 *Nicotiana tabacum*  
'peroxidase'.

AAA34108.1 J02979 *Nicotiana tabacum*  
lignin-forming peroxidase precursor (EC 1.11.1.7).

AAA33127.1 M91373 *Cucumis sativus*  
peroxidase. pre-peroxidase. putative.

BAA92500.1 AP001383 *Oryza sativa*  
ESTs D39300(R3292), AU030751(E60187) correspond to a region of the predicted gene.  
Similar to peroxidase ATP6a. (X98774).

CAB65334.1 AJ250121 *Picea abies*  
peroxidase. SPI2 protein. spi2.

CAA40796.1 X57564 *Armoracia rusticana*  
peroxidase. peroxidase precursor.

AAB06183.1 M37636 *Arachis hypogaea*  
cationic peroxidase. PNC1.

CAA76680.1 Y17192 *Cucurbita pepo*  
peroxidase. aprx. type III peroxidase.

AAA33129.1 M91372 *Cucumis sativus*  
peroxidase. pre-peroxidase.

CAA71492.1	Y10466	Spinacia oleracea
peroxidase. prx5.		
AAF63027.1	AF244924	Spinacia oleracea
hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.		
AAD43561.1	AF155124	Gossypium hirsutum
bacterial-induced peroxidase precursor. Perx_Goshiko.		
AAF63026.1	AF244923	Spinacia oleracea
hydrogen peroxide catabolism. peroxidase prx14 precursor. type III peroxidase.		
AAA33121.1	M32742	Cucumis sativus
peroxidase (CuPer2).		
BAA92422.1	AP001366	Oryza sativa
ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene.		
Similar to A.thaliana mRNA for peroxidase ATP18a. (X98804).		
BAA92497.1	AP001383	Oryza sativa
ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene.		
Similar to peroxidase ATP18a. (X98804).		
BAA77389.1	AB024439	Scutellaria baicalensis
peroxidase 3.		
BAA08499.1	D49551	Oryza sativa
peroxidase. poxN.		
AAB19129.1	U41657	Glycine max
seed coat peroxidase isozyme. SPOD4.1. H2O2 oxidoreductase.		
BAA03373.1	D14482	Oryza sativa
putative peroxidase.		
AAB02554.1	L37790	Stylosanthes humilis
cationic peroxidase.		
SEQ ID NO: 515		
AAB88134.1	AF034618	Spinacia oleracea
cytosolic heat shock 70 protein. HSC70-1.		
AAF34134.1	AF161180	Malus x domestica
high molecular weight heat shock protein. Hsp2.		
AAB99745.1	AF005993	Triticum aestivum
HSP70. TaHSP70d. 70 kDa heat shock protein, molecular chaperone.		
AAA62325.1	L32165	Hordeum vulgare
Molecular chaperone. HSP70. Heat-shock protein HSP70; The predicted amino acid sequence is highly homologous (more than 80% identity) to other plant heat-shock proteins (HSP70s) in the database; however the C terminus is quite unique.; putative.		
AAA21808.1	L23551	Spinacia oleracea
molecular chaperone. ER-lumenal protein. HSC70.		
AAA34139.1	L08830	Lycopersicon esculentum
molecular chaperon (precursor). glucose-regulated protein 78. BiP/grp78. an endoplasmic reticulum residing heat shock protein 70 family member; precursor peptide.		

AAB86942.1 AF031241 *Glycine max*  
endoplasmic reticulum transport protein; molecular chaperone; roles in protein folding, assembly, and transport. endoplasmic reticulum HSC70-cognate binding protein precursor. BIP. BiP; similar to HSC70 and GRP78.

AAK21920.1 AF338252 *Glycine max*  
molecular chaperone. BiP-isoform D. BiPD. ER-lumenal HSP70; binding protein GRP78.

AAB91473.1 AF035458 *Spinacia oleracea*  
heat shock 70 protein. HSC70-11. mitochondrial protein.

AAB96660.1 AF039084 *Spinacia oleracea*  
heat shock 70 protein. HSC70-11. molecular chaperone.

AAB91472.1 AF035457 *Spinacia oleracea*  
heat shock 70 protein. HSC70-10. mitochondrial protein.

SEQ ID NO: 516

CAA06927.1 AJ006233 *Nicotiana tabacum*  
putative thaumatin-like protein precursor.

AAF06346.1 AF195653 *Vitis vinifera*  
SCUTL1. thaumatin-like protein.

BAA28872.1 AB006009 *Pyrus pyrifolia*  
thaumatin-like protein precursor. PsTL1.

CAC10270.1 AJ243427 *Malus x domestica*  
thaumatin-like protein. tl. allergen, pathogenesis-related.

AAC36740.1 AF090143 *Malus x domestica*  
thaumatin-like protein precursor Mdtl1. MDTL1. pathogenesis-related.

CAB62167.1 AJ242828 *Castanea sativa*  
antifungal. thaumatin-like protein. tl1.

AAB38064.1 U32440 *Prunus avium*  
thaumatin-like protein precursor.

BAA74546.2 AB000834 *Nicotiana tabacum*  
thaumatin-like protein SE39b.

AAF06347.1 AF195654 *Vitis vinifera*  
SCUTL2. thaumatin-like protein.

CAC09477.1 AL442113 *Oryza sativa*  
thaumatin-like protein. H0806H05.10.

AAB95118.1 U71244 *Brassica rapa*  
pathogenesis-related group 5 protein. BFTP. thaumatin-like protein; PR-5.

CAA10492.1 AJ131731 *Pseudotsuga menziesii*  
Thaumatin-like protein. 5A1A.16.

BAA95017.1 AB031870 *Cestrum elegans*  
thaumatin-like protein. CETLP.

BAA95165.1 AB029918 *Nicotiana tabacum*  
pistil transmitting tissue specific thaumatin (SE39b)-like protein. SE39b.

AAB61590.1 AF003007 *Vitis vinifera*  
VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.

AAD55090.1 AF178653 *Vitis riparia*  
thaumatin, osmotin; pathogenesis-related protein.

CAB85637.1 AJ237999 *Vitis vinifera*  
putative thaumatin-like protein. T11. alternative name grip 51.

AAF82264.1 AF227324 *Vitis vinifera*  
thaumatin-like protein.

AAB02259.1 U57787 *Avena sativa*  
permatin precursor, thaumatin-like protein.

AAB53368.1 U77657 *Oryza sativa*  
pathogenesis-related thaumatin-like protein.

CAA09228.1 AJ010501 *Cicer arietinum*  
thaumatin-like protein PR-5b.

CAA33293.1 X15224 *Nicotiana tabacum*  
thaumatin-like protein. E22.

CAA33292.1 X15223 *Nicotiana tabacum*  
thaumatin-like protein. E2.

SEQ ID NO: 517

CAA71801.1 Y10848 *Brassica juncea*  
gamma-glutamylcysteine synthetase. gsh1.

AAB71230.1 AF017983 *Lycopersicon esculentum*  
gamma-glutamylcysteine synthetase. GSH1.

AAC82334.1 AF041340 *Medicago truncatula*  
gamma-glutamylcysteine synthetase. putative plastid protein.

AAF22137.1 AF128455 *Pisum sativum*  
gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.

AAF22136.1 AF128454 *Phaseolus vulgaris*  
gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.

CAA06613.1 AJ005587 *Brassica juncea*  
gamma-glutamylcysteine synthetase.

AAG13459.1 AF128453 *Glycine max*  
gamma-glutamylcysteine synthetase precursor. gsh1.

CAA64808.1 X95563 *Brassica juncea*  
gamma-glutamylcysteine synthetase. gsh1.

SEQ ID NO: 518

AAA75414.1 L28005 *Glycine max*  
TGACG-motif-binding protein. STGA1.

AAB31250.2 S73827 *Solanum tuberosum*  
mas-binding factor MBF3. transcription factor TGA1a homolog; This sequence comes from Fig. 4.

AAB31249.1 S73826 *Solanum tuberosum*  
mas-binding factor MBF2. mas-binding factor MBF2. transcription factor TGA1a homolog; This sequence comes from Fig. 4.

CAA34468.1	X16449	Nicotiana sp.
TGA1a protein (AA 1-359).		
AAA34091.1	M62855	Nicotiana tabacum
ASF-1/G13. leucine-zipper DNA-binding protein.		
AAB31251.2	S73828	Solanum tuberosum
mas-binding factor MBF1. transcription factor TGA1a homolog; This sequence comes from Fig. 4.		
CAA48904.1	X69152	Zea mays
ocs-element binding factor 3.2. OBF3.2.		
CAA48905.1	X69153	Zea mays
ocs-element binding factor 3.1. OBF3.1.		
AAC24123.1	AF067187	Cichorium intybus
cAMP responsive element binding protein. bZIP transcription factor; CREB.		
AAC24122.1	AF067186	Cichorium intybus
cAMP responsive element binding protein. CREB1.		
AAC49760.1	AF001454	Helianthus annuus
Dc3 promoter-binding factor-2. DPBF-2.		
SEQ ID NO: 521		
CAA10608.1	AJ132228	Ricinus communis
amino acid carrier. aap3.		
CAA07563.1	AJ007574	Ricinus communis
amino acid carrier. aap1.		
CAA70778.1	Y09591	Vicia faba
amino acid transporter.		
AAD16014.1	AF080543	Nepenthes alata
amino acid transporter. AAP2.		
CAA70969.1	Y09826	Solanum tuberosum
amino acid transporter. AAP2. transmembrane protein.		
AAD16015.1	AF080544	Nepenthes alata
amino acid transporter. AAP3.		
CAA70968.1	Y09825	Solanum tuberosum
amino acid transporter. AAP1. transmembrane protein.		
CAA92992.1	Z68759	Ricinus communis
amino acid carrier.		
AAD16013.1	AF080542	Nepenthes alata
amino acid transporter. AAP1.		
AAF15945.1	AF061435	Vicia faba
amino acid transporter b. AAPB.		
CAA72006.1	Y11121	Ricinus communis
amino acid carrier.		
AAF15944.1	AF061434	Vicia faba
amino acid transporter a. AAPA.		

AAF15946.1 AF061436 *Vicia faba*  
amino acid transporter c. AAPC.

AAB48944.1 U31932 *Nicotiana sylvestris*  
amino acid permease 1. NSAAP1. amino acid transporter; Method: conceptual translation  
supplied by author.

AAB96830.1 U64823 *Nicotiana sylvestris*  
amino acid transporter. amino acid permease. nsaap1.

BAA93437.1 AB022783 *Oryza sativa*  
amino acid permease. OsproT.

AAD25162.1 AF014810 *Lycopersicon esculentum*  
proline transporter 3. LeProT3.

AAD25161.1 AF014809 *Lycopersicon esculentum*  
proline transporter 2. LeProT2.

AAD25160.1 AF014808 *Lycopersicon esculentum*  
proline transporter 1. LeProT1.

AAF76897.1 AF274032 *Atriplex hortensis*  
proline/glycine betaine transporter.

CAB42599.1 AJ238635 *Chlorella protothecoides*  
amino acid carrier. dee4.

SEQ ID NO: 526

BAA03763.1 D16247 *Nicotiana sylvestris*  
RNA helicase like protein DB10.

AAD46404.1 AF096248 *Lycopersicon esculentum*  
ethylene-responsive RNA helicase. ER68. putative DEAD box/RNA helicase.

AAF75791.1 AF271892 *Pisum sativum*  
DEAD box protein P68. P68. RNA helicase.

AAF40306.1 AF156667 *Vigna radiata*  
RNA helicase. VRH1.

CAA68193.1 X99937 *Spinacia oleracea*  
RNA helicase. prh75. DEAD-box protein; homologous to X99938.

AAG13612.1 AC078840 *Oryza sativa*  
putative RNA helicase. OSJNBb0073N24.12.

AAG34876.1 AF261021 *Nicotiana tabacum*  
putative chloroplast RNA helicase VDL isoform 1. VDL. alternatively spliced.

AAG34873.1 AF261020 *Nicotiana tabacum*  
putative chloroplast RNA helicase VDL isoform 1. VDL. essential for chloroplast  
development; may be involved in post-transcriptional regulation.

AAG34879.1 AF261024 *Nicotiana tabacum*  
putative chloroplast RNA helicase VDL' isoform 1. VDL'. alternatively spliced.

AAD20980.1 AF079782 *Zea mays*  
ATPase and RNA helicase. translation initiation factor 4A2. tif4A2.

AAG34882.1 AF261027 *Nicotiana tabacum*  
putative chloroplast RNA helicase VDL' isoform 4. VDL'. alternatively spliced.

BAA95705.1	AB042644	Oryza sativa DEAD box RNA helicase OsPL10b. OsPL10b.
BAA95704.1	AB042643	Oryza sativa DEAD box RNA helicase OsPL10a. OsPL10a.
AAG34883.1	AF261028	Nicotiana tabacum putative chloroplast RNA helicase VDL' isoform 5. VDL'. alternatively spliced.
AAG38493.1	AF261032	Nicotiana tabacum putative chloroplast RNA helicase VDL' isoform 1. VDL'. alternatively spliced.
AAG34884.1	AF261029	Nicotiana tabacum putative chloroplast RNA helicase VDL' isoform 6. VDL'. alternatively spliced.
AAG38496.1	AF261032	Nicotiana tabacum putative chloroplast RNA helicase VDL' isoform 4. VDL'. alternatively spliced.
AAG38497.1	AF261032	Nicotiana tabacum putative chloroplast RNA helicase VDL' isoform 5. VDL'. alternatively spliced.
AAG38498.1	AF261032	Nicotiana tabacum putative chloroplast RNA helicase VDL' isoform 6. VDL'. alternatively spliced.
AAG38500.1	AF261032	Nicotiana tabacum putative chloroplast RNA helicase VDL' isoform 8. VDL'. alternatively spliced.
AAG34886.1	AF261031	Nicotiana tabacum putative chloroplast RNA helicase VDL' isoform 8. VDL'. alternatively spliced.
AAG48833.1	AC084218	Oryza sativa similar to <i>Arabidopsis thaliana</i> DNA helicase (AJ404475).
SEQ ID NO: 528		
CAA65536.1	X96761	<i>Sporobolus stapfianus</i> sulphate transporter protein.
AAK27688.1	AF347614	<i>Lycopersicon esculentum</i> sulfate transporter 2. ST2.
AAK27687.1	AF347613	<i>Lycopersicon esculentum</i> sulfate transporter 1. ST1.
CAA57711.1	X82256	<i>Stylosanthes hamata</i> high affinity sulphate transporter. SHST2.
AAG41419.1	AF309643	<i>Solanum tuberosum</i> high affinity sulfate transporter type 1. ST1.
CAA57710.1	X82255	<i>Stylosanthes hamata</i> high affinity sulphate transporter. SHST1.
AAK35215.1	AF355602	<i>Zea mays</i> sulfate transporter ST1.
CAA65291.1	X96431	<i>Hordeum vulgare</i> high affinity sulphate transporter. HVST1.
AAA97952.1	U52867	<i>Hordeum vulgare</i> high affinity sulfate transporter HVST1.

CAB42985.1 AJ238244 *Aegilops tauschii*  
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st1.

CAB42986.1 AJ238245 *Aegilops tauschii*  
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st2.

CAA57831.1 X82454 *Stylosanthes hamata*  
low affinity sulphate transporter. SHST3.

SEQ ID NO: 531

AAK00436.1 AC060755 *Oryza sativa*  
putative zinc finger protein. OSJNBA0003O19.23.

BAA85438.1 AP000616 *Oryza sativa*  
similar to RING-H2 finger protein RHA1a (AF078683).

AAG43550.1 AF211532 *Nicotiana tabacum*  
Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

BAA90357.1 AP001080 *Oryza sativa*  
EST AU070319(S10788) corresponds to a region of the predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).

SEQ ID NO: 532

BAA81751.1 AB017517 *Marchantia polymorpha*  
calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.

BAA13232.1 D87042 *Zea mays*  
Calcium-dependent protein kinase.

BAA81749.1 AB017515 *Marchantia polymorpha*  
calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.

BAA81750.1 AB017516 *Marchantia polymorpha*  
calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.

BAA85396.1 AP000615 *Oryza sativa*  
ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844)  
correspond to a region of the predicted gene.; similar to calcium dependent protein kinase.  
(AF048691).

CAA57156.1 X81393 *Oryza sativa*  
calcium-dependent protein kinase. OSCPKII.

AAC05270.1 AF048691 *Oryza sativa*  
calcium dependent protein kinase. CDPK12.

AAB49984.1 U90262 *Cucurbita pepo*  
calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine  
protein kinase that is activated by direct binding of calcium.

AAB70706.1 U82087 *Tortula ruralis*  
calmodulin-like domain protein kinase. TrCPK1.

AAG46110.1 AC073166 *Oryza sativa*  
calcium-dependent protein kinase. OSJNBB0064P21.2.

BAA02698.1 D13436 *Oryza sativa*  
calcium-dependent protein kinase. spk.

BAA81748.1 AB017515 *Marchantia polymorpha*  
calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.

CAA07481.1 AJ007366 *Zea mays*  
calcium-dependent protein kinase.

AAB80692.1 U69173 *Glycine max*  
calmodulin-like domain protein kinase isoenzyme beta. CDPK beta.

AAC49405.1 U08140 *Vigna radiata*  
calcium dependent protein kinase. CDPK.

BAA12338.1 D84408 *Zea mays*  
calcium dependent protein kinase. ZmCDPK1.

AAA33443.1 L15390 *Zea mays*  
calcium-dependent protein kinase. CDPK.

CAA57157.1 X81394 *Oryza sativa*  
calcium-dependent protein kinase. OSCPK2.

BAB21081.1 AP002819 *Oryza sativa*  
putative calcium-dependent protein kinase. P0501G01.10.

BAA12715.1 D85039 *Zea mays*  
calcium-dependent protein kinase.

CAA65500.1 X96723 *Medicago sativa*  
protein kinase. CDPK.

AAC25423.1 AF072908 *Nicotiana tabacum*  
calcium-dependent protein kinase. CDPK1.

AAA69507.1 U28376 *Zea mays*  
calcium-dependent protein kinase. MZECDPK2.

BAA13440.1 D87707 *Ipomoea batatas*  
calcium dependent protein kinase. CDPK.

AAD28192.2 AF115406 *Solanum tuberosum*  
calcium-dependent protein kinase. CDPK; catalytic domain.

AAB80693.1 U69174 *Glycine max*  
calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.

AAA61682.1 L27484 *Zea mays*  
calcium-dependent protein kinase. CDPK.

AAD17800.1 AF090835 *Mesembryanthemum crystallinum*  
Ca2+-dependent protein kinase. CPK1. serine/threonine protein kinase.

CAA39936.1 X56599 *Daucus carota*  
calcium- dependent protein kinase. DcPK431.

AAK26164.1 AY027885 *Cucumis sativus*  
calcium-dependent calmodulin-independent protein kinase 5. CDPK5. CsCDPK5.

AAB88537.1 AF035944 *Fragaria x ananassa*  
calcium-dependent protein kinase. MAX17.

AAF21062.1 AF216527 *Dunaliella tertiolecta*  
calcium-dependent protein kinase. CPK1; CDPK.

CAA89202.1	Z49233	Chlamydomonas eugametos calcium-stimulated protein kinase.
AAC32116.1	AF051211	Picea mariana probable calcium dependent protein kinase. Sb15. similar to Vigna radiata calcium dependent protein kinase encoded by U08140.
AAF23900.1	AF194413	Oryza sativa calcium-dependent protein kinase. CDPK1. OsCDPK1.
AAF23901.2	AF194414	Oryza sativa calcium-dependent protein kinase. CDPK5. OsCDPK5.
CAB46228.1	Y18055	Arachis hypogaea calcium dependent protein kinase. CDPK.
AAC78558.1	AF030879	Solanum tuberosum protein kinase CPK1.
CAA58750.1	X83869	Daucus carota CDPK-related protein kinase. CRK (or PK421).
AAB47181.1	S82324	Zea mays /gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.
BAA12691.1	D84507	Zea mays CDPK-related protein kinase. Does not require calcium for its activity (by similarity).
BAA22410.1	D38452	Zea mays calcium-dependent protein kinase-related kinase.
BAA12692.1	D84508	Zea mays CDPK-related protein kinase. Does not require calcium for its activity.
AAG01179.1	AF289237	Zea mays calcium/calmodulin dependent protein kinase MCK2. MCK2.
AAC24961.1	AF009337	Tradescantia virginiana CDPK-related protein kinase. CRK1.
BAA90814.1	AP001168	Oryza sativa ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
AAC49008.1	U24188	Lilium longiflorum calcium/calmodulin-dependent phosphorylation activity. calcium/calmodulin-dependent protein kinase. CCaMK. serine/threonine kinase; binds to calcium and calmodulin.
AAF19402.1	AF203480	Lycopersicon esculentum phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.
SEQ ID NO: 535		
AAK19619.1	AF336286	Gossypium hirsutum GHMYB9. ghmyb9. similar to myb.
CAA64614.1	X95296	Lycopersicon esculentum transcription factor. THM27. myb-related.
CAA50224.1	X70879	Hordeum vulgare MybHv1. myb1.

CAA50222.1	X70877	Hordeum vulgare
MybHv1.	myb1.	
AAA33067.1	L04497	Gossypium hirsutum
MYB A;	putative.	
CAA50221.1	X70876	Hordeum vulgare
MybHv5.	myb2.	
BAA23337.1	D88617	Oryza sativa
transfactor.	OSMYB1.	Osmyb1.
BAA23338.1	D88618	Oryza sativa
transfactor.	OSMYB2.	Osmyb2.
AAC04720.1	AF034134	Gossypium hirsutum
putative MYB-like transcription factor.	MYB-like DNA-binding domain protein.	Cmy-O.
similar to MYB A	encoded by GenBank Accession Number	L04497.
CAA72218.1	Y11415	Oryza sativa
myb.		
CAA50225.1	X70880	Hordeum vulgare
MybHv5.	myb2.	
AAA82943.1	U39448	Picea mariana
MYB-like transcriptional factor MBF1.	putative DNA binding region	highly similar to the maize C1.
CAA78386.1	Z13996	Petunia x hybrida
DNA binding protein; transcriptional activator.	protein 1.	myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
BAA81732.1	AB029161	Glycine max
GmMYB29A2.		
AAK19616.1	AF336283	Gossypium hirsutum
GHMYB25.	ghmyb25.	similar to myb; contains an unspliced intron.
AAK19611.1	AF336278	Gossypium hirsutum
BNLGH1233.	bnlghi6233.	similar to myb.
AAK19617.1	AF336284	Gossypium hirsutum
GHMYB36.	ghmyb36.	similar to myb.
BAA93038.1	AP001552	Oryza sativa
EST AU082058(C12976)	corresponds to a region of the predicted gene.	Similar to Arabidopsis thaliana putative transcription factor (AF062916).
AAK19615.1	AF336282	Gossypium hirsutum
GHMYB10.	ghmyb10.	similar to myb.
BAB39987.1	AP003020	Oryza sativa
putative transcription factor (myb).	P0498A12.16.	contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa
putative transcription factor (myb).	OSJNBA0004B13.27.	contains ESTs AU097474(S5087),D40175(S1959).

CAB43399.1 AJ006292 *Antirrhinum majus*  
Myb-related transcription factor mixta-like 1. mybml1.

CAA72185.1 Y11350 *Oryza sativa*  
myb factor. myb.

AAF22256.1 AF161711 *Pimpinella brachycarpa*  
myb-related transcription factor.

AAG13574.1 AC037425 *Oryza sativa*  
myb factor. OSJNBa0055P24.4.

BAA81731.1 AB029160 *Glycine max*  
GmMYB29A1.

BAA81730.1 AB029159 *Glycine max*  
GmMYB29A1.

CAA72186.1 Y11351 *Oryza sativa*  
myb factor. myb.

CAA67600.1 X99210 *Lycopersicon esculentum*  
myb-related transcription factor. THM16.

CAA75509.1 Y15219 *Oryza sativa* subsp. *indica*  
transcriptional activator. C1.

AAC04718.1 AF034132 *Gossypium hirsutum*  
putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-J.  
similar to MYB A encoded by GenBank Accession Number L04497.

CAA78387.1 Z13997 *Petunia x hybrida*  
DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb  
proto-oncoproteins.

BAA81736.1 AB029165 *Glycine max*  
GmMYB29B2.

AAK19618.1 AF336285 *Gossypium hirsutum*  
GHMYB38. ghmyb38. similar to myb.

CAA72217.1 Y11414 *Oryza sativa*  
myb.

AAC49394.1 U57002 *Zea mays*  
P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the  
C-terminal.

AAA33500.1 M73028 *Zea mays*  
myb-like transcription factor. P.

BAB20661.1 AP002871 *Oryza sativa*  
putative myb-related protein P. P0475H04.31.

AAG36774.1 AF210616 *Zea mays*  
P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.

BAA88222.1 AB028650 *Nicotiana tabacum*  
myb-related transcription factor LBM2. lbm2.

BAA81733.2 AB029162 *Glycine max*  
GmMYB29A2.

BAA23339.1 D88619 *Oryza sativa*  
transfactor. OSMYB3. Osmyb3.

BAA88224.1 AB028652 *Nicotiana tabacum*  
myb-related transcription factor LBM4. lbm4.

BAA88221.1 AB028649 *Nicotiana tabacum*  
myb-related transcription factor LBM1. lbm1.

AAB41101.1 U72762 *Nicotiana tabacum*  
transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.

SEQ ID NO: 536

CAA70968.1 Y09825 *Solanum tuberosum*  
amino acid transporter. AAP1. transmembrane protein.

AAF15946.1 AF061436 *Vicia faba*  
amino acid transporter c. AAPC.

CAA70969.1 Y09826 *Solanum tuberosum*  
amino acid transporter. AAP2. transmembrane protein.

AAB96830.1 U64823 *Nicotiana sylvestris*  
amino acid transporter. amino acid permease. nsaap1.

CAA07563.1 AJ007574 *Ricinus communis*  
amino acid carrier. aap1.

AAB48944.1 U31932 *Nicotiana sylvestris*  
amino acid permease 1. NSAAP1. amino acid transporter; Method: conceptual translation supplied by author.

AAD16015.1 AF080544 *Nepenthes alata*  
amino acid transporter. AAP3.

CAA70778.1 Y09591 *Vicia faba*  
amino acid transporter.

AAF15944.1 AF061434 *Vicia faba*  
amino acid transporter a. AAPA.

AAF15945.1 AF061435 *Vicia faba*  
amino acid transporter b. AAPB.

AAF76897.1 AF274032 *Atriplex hortensis*  
proline/glycine betaine transporter.

AAD16014.1 AF080543 *Nepenthes alata*  
amino acid transporter. AAP2.

AAD25161.1 AF014809 *Lycopersicon esculentum*  
proline transporter 2. LeProT2.

CAA10608.1 AJ132228 *Ricinus communis*  
amino acid carrier. aap3.

SEQ ID NO: 537

BAA89009.1 AB027455 *Petunia x hybrida*  
anthocyanin 5-O-glucosyltransferase. PH1.

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BAA36423.1 AB013598 *Verbena x hybrida*  
UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

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BAA36421.1 AB013596 *Perilla frutescens*  
UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.

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BAB07962.1 AP002524 *Oryza sativa*  
putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs  
AU067881(C10481),AU067882(C10481).

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BAA36422.1 AB013597 *Perilla frutescens*  
UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.

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BAA93039.1 AB033758 *Citrus unshiu*  
limonoid UDP-glucosyltransferase. LGTase.

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AAF61647.1 AF190634 *Nicotiana tabacum*  
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

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AAF98390.1 AF287143 *Brassica napus*  
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other  
hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate  
glucosyltransferase. SGT1. SGT.

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AAK16175.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBA0040E01.15.

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AAF17077.1 AF199453 *Sorghum bicolor*  
UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-  
glucosyltransferase.

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AAK16172.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBA0040E01.14.

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BAA83484.1 AB031274 *Scutellaria baicalensis*  
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

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AAK16181.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBA0040E01.16.

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AAG25643.1 AF303396 *Phaseolus vulgaris*  
UDP-glucosyltransferase HRA25. putative; defense associated.

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AAK16178.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBA0040E01.5.

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AAD21086.1 AF127218 *Forsythia x intermedia*  
adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-  
glucosyltransferase. UFGT.

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BAA12737.1 D85186 *Gentiana triflora*  
UDP-glucose:flavonoid-3-glucosyltransferase.

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AAK28303.1 AF346431 *Nicotiana tabacum*  
phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.

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CAB56231.1 Y18871 *Dorotheanthus bellidiformis*  
betanidin-5-O-glucosyltransferase.

---

CAA54612.1 X77462 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT5.

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BAB41019.1	AB047092	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41020.1	AB047093	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
AAB36653.1	U32644	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS5a.
BAB41025.1	AB047098	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FlUFGT1.
BAB41023.1	AB047096	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT1.
BAB41022.1	AB047095	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41021.1	AB047094	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAA19659.1	AB002818	Perilla frutescens flavonoid 3-O-glucosyltransferase. UDP glucose.
BAB41026.1	AB047099	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FlUFGT2.
BAB41024.1	AB047097	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT2.
AAK16180.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBA0040E01.21.
AAK28304.1	AF346432	Nicotiana tabacum phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.
AAB36652.1	U32643	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS10a.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAA89008.1	AB027454	Petunia x hybrida anthocyanidin 3-O-glucosyltransferase. PGT8.
CAA59450.1	X85138	Lycopersicon esculentum twi1. homologous to glucosyltransferases.
CAA54614.1	X77464	Manihot esculenta UTP-glucose glucosyltransferase. CGT7.
CAA54611.1	X77461	Manihot esculenta UTP-glucose glucosyltransferase. CGT2.
CAA54613.1	X77463	Manihot esculenta UTP-glucose glucosyltransferase. CGT6.
SEQ ID NO: 540		
AAK27688.1	AF347614	Lycopersicon esculentum sulfate transporter 2. ST2.

AAG41419.1 AF309643 *Solanum tuberosum*  
high affinity sulfate transporter type 1. ST1.

AAK27687.1 AF347613 *Lycopersicon esculentum*  
sulfate transporter 1. ST1.

AAA97952.1 U52867 *Hordeum vulgare*  
high affinity sulfate transporter HVST1.

CAA57711.1 X82256 *Stylosanthes hamata*  
high affinity sulphate transporter. SHST2.

CAA65291.1 X96431 *Hordeum vulgare*  
high affinity sulphate transporter. HVST1.

CAA57710.1 X82255 *Stylosanthes hamata*  
high affinity sulphate transporter. SHST1.

CAB42985.1 AJ238244 *Aegilops tauschii*  
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st1.

AAK35215.1 AF355602 *Zea mays*  
sulfate transporter ST1.

CAB42986.1 AJ238245 *Aegilops tauschii*  
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st2.

CAA65536.1 X96761 *Sporobolus stapfianus*  
sulphate transporter protein.

CAA57831.1 X82454 *Stylosanthes hamata*  
low affinity sulphate transporter. SHST3.

CAA11413.1 AJ223495 *Brassica juncea*  
sulfate permease. sp1.

AAB94543.1 AF016306 *Zea mays*  
sulfate permease.

SEQ ID NO: 541

AAF36491.1 AF129479 *Hordeum vulgare*  
HAK2. HAK2. similar to *Hordeum vulgare* K<sup>+</sup> transporter HAK1.

BAB32443.1 AB055630 *Phragmites australis*  
high-affinity potassium transporter. PcnHAK1.

BAB32444.1 AB055631 *Phragmites australis*  
high-affinity potassium transporter. PceHAK1A.

BAB32445.1 AB055632 *Phragmites australis*  
high-affinity potassium transporter. PceHAK1B.

BAB32442.1 AB055629 *Phragmites australis*  
high-affinity potassium transporter. PcuHAK1.

AAC39315.1 AF025292 *Hordeum vulgare*  
putative high-affinity potassium transporter. HvHAK1.

AAF36497.1 AF129485 *Oryza sativa*  
HAK4. HAK4. OsHAK4; similar to *Hordeum vulgare* K<sup>+</sup> transporter HAK1.

AAF36496.1 AF129484 *Hordeum vulgare*  
HAK4. HAK4. HvHAK4; similar to *Hordeum vulgare* K<sup>+</sup> transporter HAK1.

CAC14883.1 AJ297888 *Hordeum vulgare*  
putative potassium transporter. hak1.

CAC14787.1 AJ297886 *Hordeum vulgare*  
putative potassium transporter. hak1.

AAF36492.1 AF129480 *Hordeum vulgare*  
HAK1B. HAK1B. HvHAK1B; similar to *Hordeum vulgare* K<sup>+</sup> transporter HAK1.

CAC15061.1 AJ300161 *Hordeum vulgare*  
potassium transporter. hak4.

SEQ ID NO: 542

AAA91063.1 M88254 *Hevea brasiliensis*  
ethylene-inducible protein. ER1.

SEQ ID NO: 546

CAA75386.1 Y15113 *Morinda citrifolia*  
3-deoxy-D-arabino-heptulosonate 7-phosphate synthase. DS3. 2-dehydro-3-deoxyphosphoheptonate aldolase.

CAA79855.1 Z21792 *Lycopersicon esculentum*  
phospho-2-dehydro-3-deoxyheptonate aldolase.

CAA79856.1 Z21793 *Lycopersicon esculentum*  
phospho-2-dehydro-3-deoxyheptonate aldolase.

SEQ ID NO: 548

BAA96751.1 AP002521 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome4, BAC clone T16H5; lectin like protein (AL024486).

SEQ ID NO: 551

BAB19096.1 AP002839 *Oryza sativa*  
putative DNA-binding protein homolog. P0688A04.2.

BAB19075.1 AP002744 *Oryza sativa*  
putative DNA-binding protein homolog. P0006C01.17.

AAK16170.1 AC079887 *Oryza sativa*  
putative DNA binding protein. OSJNBa0040E01.4.

AAD32677.1 AF140554 *Avena sativa*  
DNA-binding protein WRKY1. wrky1. putative transcription factor.

AAD16139.1 AF096299 *Nicotiana tabacum*  
DNA-binding protein 2. WRKY2. transcription factor.

CAB97004.1 AJ278507 *Solanum tuberosum*  
putative transcription factor. WRKY DNA binding protein. WRKY1.

CAA88326.1 Z48429 *Avena fatua*  
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

AAC49527.1 U48831 *Petroselinum crispum*  
WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

AAC49529.1	U58540	Petroselinum crispum WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAK16171.1	AC079887	Oryza sativa putative DNA-binding protein. OSJNBa0040E01.10.
AAC37515.1	L44134	Cucumis sativus SPF1-like DNA-binding protein.
AAD16138.1	AF096298	Nicotiana tabacum DNA-binding protein 1. WRKY1. transcription factor.
AAD38283.1	AC007789	Oryza sativa putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB18313.1	AP002865	Oryza sativa putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
BAB40073.1	AP003074	Oryza sativa putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAC49528.1	U56834	Petroselinum crispum DNA-binding. WRKY3. WRKY-type DNA-binding protein.
BAA77358.1	AB020023	Nicotiana tabacum WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG46150.1	AC018727	Oryza sativa putative DNA-binding protein. OSJNBa0056G17.18.
CAA88331.1	Z48431	Avena fatua binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD32676.1	AF140553	Avena sativa DNA-binding protein WRKY3. wrky3. putative transcription factor.
CAB66338.1	AJ279697	Betula pendula wrky-type DNA binding protein. wrky.
AAF61863.1	AF193770	Nicotiana tabacum DNA-binding protein 3. WRKY3. transcription factor.
AAF61864.1	AF193771	Nicotiana tabacum DNA-binding protein 4. WRKY4. transcription factor.
AAD27591.1	AF121354	Petroselinum crispum binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
BAA87069.1	AB035271	Matricaria chamomilla elicitor-induced DNA-binding protein homolog. McWRKY1.
SEQ ID NO: 553		
AAF34428.1	AF172282	Oryza sativa receptor-like protein kinase. DUPR11.18.
BAA94518.1	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAB07904.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.12.

BAA94516.1 AP001800 Oryza sativa  
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).

BAB07906.1 AP002835 Oryza sativa  
putative S-receptor kinase. P0417G05.14.

BAA94517.1 AP001800 Oryza sativa  
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).

BAB07905.1 AP002835 Oryza sativa  
putative S-receptor kinase. P0417G05.13.

BAA94528.1 AP001800 Oryza sativa  
Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).

BAA94529.2 AP001800 Oryza sativa  
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).

CAA67145.1 X98520 Brassica oleracea  
receptor-like kinase. SFR2.

CAA73133.1 Y12530 Brassica oleracea  
serine /threonine kinase. ARLK.

CAB89179.1 AJ245479 Brassica napus subsp. napus  
ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 Brassica napus  
serine/threonine kinase receptor.

AAC23542.1 U20948 Ipomoea trifida  
receptor protein kinase. IRK1.

BAA23676.1 AB000970 Brassica rapa  
receptor kinase 1. BcRK1.

BAA92836.1 AB032473 Brassica oleracea  
S18 S-locus receptor kinase. SRK18.

CAB41878.1 Y18259 Brassica oleracea  
SRK5 protein. SRK5. receptor-like kinase.

CAB41879.1 Y18260 Brassica oleracea  
SRK15 protein. SRK15. receptor-like kinase.

BAA21132.1 D88193 Brassica rapa  
S-receptor kinase. SRK9 (B.c.).

BAA06285.1 D30049 Brassica rapa  
S-receptor kinase SRK9.

CAA74662.1 Y14286 Brassica oleracea  
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

CAA79355.1 Z18921 Brassica oleracea  
S-receptor kinase-like protein.

BAB21001.1 AB054061 Brassica rapa  
S locus receptor kinase. SRK22.

AAA33915.1 L27821 Oryza sativa  
receptor type serine/threonine kinase. protein kinase.

BAA92954.1 AP001551 Oryza sativa  
Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).

SEQ ID NO: 554

CAC05658.1 AJ250919 Brassica napus  
endopolygalacturonase. pegaz.

CAC05657.1 AJ250918 Brassica napus  
endopolygalacturonase. pgaz.

CAA65072.1 X95800 Brassica napus  
polygalacturonase.

CAA90272.1 Z49971 Brassica napus  
Hydrolytic enzyme. Polygalacturonase. pga.

CAA54448.1 X77231 Prunus persica  
polygalacturonase. PG.

AAC14453.1 L12019 Actinidia deliciosa  
polygalacturonase.

AAF71160.1 AF152758 Actinidia chinensis  
polygalacturonase A. PGA.

AAA34178.1 M37304 Lycopersicon esculentum  
polygalacturonase.

CAA32235.1 X14074 Lycopersicon esculentum  
polygalacturonase.

CAA29148.1 X05656 Lycopersicon esculentum  
polygalacturonase (AA 1-457).

AAA32914.1 L06094 Persea americana  
cell wall degradation. polygalacturonase.

CAA47055.1 X66426 Persea americana  
polygalacturonase.

AAC26512.1 AF062467 Cucumis melo  
polygalacturonase precursor. MPG3.

CAA11846.1 AJ224147 Rubus idaeus  
polygalacturonase. RAS3.

AAF61444.1 AF138858 Lycopersicon esculentum  
hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.

BAA88472.1 AB035890 Cucumis sativus  
polygalacturonase. CUPG1.

AAD46483.1 AF128266 Glycine max  
polygalacturonase PG1.

AAD46484.1 AF128267 Glycine max  
polygalacturonase PG2.

AAC28905.1 AF001002 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4.  
TAPG4. expressed in abscission.

AAC28906.1 AF001003 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5.  
TAPG5. expressed in abscission.

AAC28903.1 AF001000 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1.  
TAPG1. expressed in abscission.

AAA80489.1 U23053 *Lycopersicon esculentum*  
polygalacturonase precursor.

AAC64184.1 AF095577 *Prunus persica*  
endopolygalacturonase.

AAC28902.2 AF000999 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3.  
TAPG3. expressed in abscission.

AAB09575.1 U70480 *Lycopersicon esculentum*  
abscission polygalacturonase. TAPG2.

AAC28904.1 AF001001 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2.  
TAPG2. expressed in abscission.

CAA54150.1 X76735 *Prunus persica*  
endopolygalacturonase.

AAC70951.1 AF072732 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and  
abundantly expressed in pistils.

AAC26511.1 AF062466 *Cucumis melo*  
polygalacturonase precursor. MPG2.

AAB09576.1 U70481 *Lycopersicon esculentum*  
abscission polygalacturonase. TAPG4.

AAC28947.1 AF029230 *Lycopersicon esculentum*  
polygalacturonase. TPG6.

AAA82167.1 U09717 *Gossypium hirsutum*  
polygalacturonase.

AAA58322.1 U09805 *Gossypium barbadense*  
polygalacturonase.

CAA47052.1 X66422 *Zea mays*  
polygalacturonase. PG.

AAG14416.1 AF248538 *Nicotiana tabacum*  
NTS1 protein. similar to polygalacturonase.

CAB42886.1 AJ238848 *Phleum pratense*  
polygalacturonase. pg.

CAA40850.1	X57627	Zea mays polygalacturonase.
CAA46679.1	X65844	Zea mays polygalacturonase. PGg6.
CAA40910.1	X57743	Zea mays polygalacturonase.
CAA44249.1	X62385	Zea mays polygalacturonase.
CAA45751.1	X64408	Zea mays polygalacturonase. PG. pollen-preferentially expressed.
CAA40851.1	X57628	Zea mays polygalacturonase.
CAA46680.1	X65845	Zea mays polygalacturonase. PGg14.
AAC26510.1	AF062465	Cucumis melo polygalacturonase precursor. MPG1.
SEQ ID NO: 556		
CAA51734.1	X73301	Vigna mungo alpha-amylase. amyVm1.
CAA37217.1	X53049	Vigna mungo alpha-amylase (AA 1-421).
BAA33879.1	AB015131	Phaseolus vulgaris alpha-amylase.
AAA16513.1	U06754	Cuscuta reflexa starch hydrolysis. alpha amylase precursor. CUS AMY2.
AAA98615.1	J04202	Hordeum vulgare alpha-amylase. Amy46. precursor.
AAA98790.1	K02637	Hordeum vulgare alpha-amylase type B. Amy6-4. precursor.
CAA33298.1	X15226	Hordeum vulgare alpha-amylase.
AAA33885.1	M24286	Oryza sativa alpha-amylase (EC 3.2.1.1).
CAA34516.1	X16509	Oryza sativa alpha-amylase.
CAA72144.1	Y11277	Hordeum vulgare alpha-amylase. amy.
CAA33299.1	X15227	Hordeum vulgare alpha amylase.
AAA32925.1	M17126	Hordeum vulgare alpha-amylase 1.

AAA32927.1	M17128	Hordeum vulgare alpha-amylase 2.
AAA32929.1	J01236	Hordeum vulgare alpha-amylase type A, EC 3.2.1.1.
CAA39777.1	X56337	Oryza sativa alpha-amylase. RAmy3B.
CAA09323.1	AJ010728	Avena fatua alpha amylase. alpha-Amy2A.
AAA33897.1	M24941	Oryza sativa alpha-amylase precursor (EC 3.2.1.1).
CAA09324.1	AJ010729	Avena fatua alpha-amylase. alpha-Amy2D.
CAA28803.1	X05166	Hordeum vulgare alpha-amylase type A. Amy32b.
AAA32926.1	M17125	Hordeum vulgare alpha-amylase 1.
CAA39778.1	X56338	Oryza sativa alpha-amylase. RAmy3C.
AAA32935.1	M15208	Hordeum vulgare alpha-amylase.
AAA33895.1	M59351	Oryza sativa alpha-amylase. RAmy3D.
AAA33896.1	M59352	Oryza sativa alpha-amylase. RAmy3E.
AAA50161.1	L25805	Zea mays alpha-amylase.
AAA33894.1	M74177	Oryza sativa alpha-amylase. amy2A.
CAA72143.1	Y11276	Hordeum vulgare alpha-amylase. amy.
CAA39776.1	X56336	Oryza sativa alpha-amylase. RAmy3A.
CAA45903.1	X64619	Oryza sativa alpha-amylase. Amyc2. starts hydrolysis during seed germination.
AAA33886.1	M24287	Oryza sativa alpha-amylase (EC 3.2.1.1).
AAA32928.1	M17127	Hordeum vulgare alpha-amylase 2.
AAA32933.1	K02638	Hordeum vulgare pre-alpha-amylase type B, EC 3.2.1.1.
AAA91883.1	M81682	Solanum tuberosum alpha-amylase. Amy23.

AAA34259.1	M16991	Triticum aestivum alpha-amylase.
CAA29252.1	X05809	Triticum aestivum alpha-amylase.
AAA91884.1	M79328	Solanum tuberosum alpha-amylase.
AAF63239.1	AF153828	Malus x domestica degrades starch. alpha-amylase. alpha-amylase by similarity.
AAA32930.1	M10056	Hordeum vulgare alpha-amylase type B, EC 3.2.1.1.
AAA32931.1	K02635	Hordeum vulgare alpha-amylase type B, EC 3.2.1.1.
CAA36485.1	X52240	Oryza sativa alpha-amylase. OSamy-c.
AAA32932.1	K02636	Hordeum vulgare alpha-amylase type B, EC 3.2.1.1.
SEQ ID NO: 557		
CAA90272.1	Z49971	Brassica napus Hydrolytic enzyme. Polygalacturonase. pga.
CAA65072.1	X95800	Brassica napus polygalacturonase.
CAA67020.1	X98373	Brassica napus endo-polygalacturonidase.
CAC05658.1	AJ250919	Brassica napus endopolygalacturonase. pegaz.
CAC05657.1	AJ250918	Brassica napus endopolygalacturonase. pgaz.
AAC14453.1	L12019	Actinidia deliciosa polygalacturonase.
AAF71160.1	AF152758	Actinidia chinensis polygalacturonase A. PGA.
CAA54448.1	X77231	Prunus persica polygalacturonase. PG.
AAA34178.1	M37304	Lycopersicon esculentum polygalacturonase.
CAA29148.1	X05656	Lycopersicon esculentum polygalacturonase (AA 1-457).
CAA32235.1	X14074	Lycopersicon esculentum polygalacturonase.
AAA32914.1	L06094	Persea americana cell wall degradation. polygalacturonase.

CAA47055.1 X66426 *Persea americana*  
polygalacturonase.

AAC26512.1 AF062467 *Cucumis melo*  
polygalacturonase precursor. MPG3.

CAA11846.1 AJ224147 *Rubus idaeus*  
polygalacturonase. RAS3.

BAA88472.1 AB035890 *Cucumis sativus*  
polygalacturonase. CUPG1.

AAF61444.1 AF138858 *Lycopersicon esculentum*  
hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.

AAA80489.1 U23053 *Lycopersicon esculentum*  
polygalacturonase precursor.

AAC28903.1 AF001000 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1.  
TAPG1. expressed in abscission.

AAB09575.1 U70480 *Lycopersicon esculentum*  
abscission polygalacturonase. TAPG2.

AAC28904.1 AF001001 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2.  
TAPG2. expressed in abscission.

AAC28905.1 AF001002 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4.  
TAPG4. expressed in abscission.

AAC64184.1 AF095577 *Prunus persica*  
endopolygalacturonase.

AAD46483.1 AF128266 *Glycine max*  
polygalacturonase PG1.

AAC28906.1 AF001003 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5.  
TAPG5. expressed in abscission.

AAD46484.1 AF128267 *Glycine max*  
polygalacturonase PG2.

CAA54150.1 X76735 *Prunus persica*  
endopolygalacturonase.

AAC26511.1 AF062466 *Cucumis melo*  
polygalacturonase precursor. MPG2.

AAC28902.2 AF000999 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3.  
TAPG3. expressed in abscission.

AAC70951.1 AF072732 *Lycopersicon esculentum*  
hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and  
abundantly expressed in pistils.

CAA47052.1	X66422	Zea mays polygalacturonase. PG.
AAC28947.1	AF029230	Lycopersicon esculentum polygalacturonase. TPG6.
AAA82167.1	U09717	Gossypium hirsutum polygalacturonase.
AAB09576.1	U70481	Lycopersicon esculentum abscission polygalacturonase. TAPG4.
CAA40910.1	X57743	Zea mays polygalacturonase.
CAA44249.1	X62385	Zea mays polygalacturonase.
CAA40850.1	X57627	Zea mays polygalacturonase.
AAG14416.1	AF248538	Nicotiana tabacum NTS1 protein. similar to polygalacturonase.
CAA46679.1	X65844	Zea mays polygalacturonase. PGg6.
AAC26510.1	AF062465	Cucumis melo polygalacturonase precursor. MPG1.
AAA58322.1	U09805	Gossypium barbadense polygalacturonase.
CAA46680.1	X65845	Zea mays polygalacturonase. PGg14.
CAA40851.1	X57628	Zea mays polygalacturonase.
CAA45751.1	X64408	Zea mays polygalacturonase. PG. pollen-preferentially expressed.
CAB42886.1	AJ238848	Phleum pratense polygalacturonase. pg.
SEQ ID NO: 559		
CAB43937.1	AJ006348	Fragaria x ananassa cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.
AAC95009.1	AF074923	Fragaria x ananassa endo-1,4-beta-glucanase precursor. Cell1. 1,4-beta-glucanohydrolase.
AAC12684.1	U76725	Pinus radiata endo-beta-1,4-glucanase. PrCell. cellulase; PRCEL1.
AAA69909.1	U13055	Lycopersicon esculentum cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel2. cellulase.
CAA65600.1	X96856	Prunus persica endo-beta-1,4-glucanase. ppEG1.

CAA65597.1	X96853	Prunus persica endo-beta-1,4-glucanase. pcel1.
CAA65827.1	X97189	Capsicum annuum endo-beta-1,4-glucanase. ccel3. cellulase.
AAC62241.1	AF077339	Lycopersicon esculentum endo-1,4-beta-glucanase. cel5. cellulase; also expressed in fruit and pistils.
BAA85150.1	AB032830	Pisum sativum endo-1,4-beta-glucanase. EGL2.
AAA80495.1	U20590	Lycopersicon esculentum endo-1,4-beta-glucanase precursor. cellulase.
BAB32662.1	AB055886	Atriplex lentiformis beta-1,4-glucanase. Al-cell1. cellulase.
CAA65828.1	X97190	Capsicum annuum endo-beta-1,4-glucanase. ccel2.
AAC12685.1	U76756	Pinus radiata endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.
BAA77239.1	AB025796	Populus alba endo-1,4-beta glucanase. POPCEL2. cellulase.
CAB59900.1	AJ010950	Capsicum annuum cell wall degradation. endo-beta-1,4-glucanase. eg2.
BAB39483.1	AB049200	Populus alba endo-1,4-beta-glucanase. PopCel2.
BAB39482.1	AB049199	Populus alba endo-1,4-beta glucanase. PopCel1.
CAA72133.1	Y11268	Lycopersicon esculentum endo-1,4-beta-D-glucanase. cel7.
AAA96135.1	L41046	Pisum sativum endo-1,4-beta-glucanase. EGL1.
AAC78504.1	U34754	Phaseolus vulgaris endo-1,4-beta-D-glucanase. cellulase.
AAA02563.1	M57400	Phaseolus vulgaris cellulase precursor. endo-1,4-beta-D-glucanase.
CAA60737.1	X87323	Capsicum annuum catalyzes hydrolysis of cell wall polysaccharides. cellulase. cell. Beta-1,4-endoglycanohydrolase.
CAA65826.1	X97188	Capsicum annuum endo-beta-1,4-glucanase. ccel1. cellulase.
AAA69908.1	U13054	Lycopersicon esculentum cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cell1. cellulase.
CAB43938.1	AJ006349	Fragaria x ananassa cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.

---

BAA96209.1 AP002094 *Oryza sativa*

EST C72268(E1328) corresponds to a region of the predicted gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).

---

BAA96207.1 AP002094 *Oryza sativa*

EST C72268(E1328) corresponds to a region of the predicted gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).

---

AAD08699.1 AF098292 *Lycopersicon esculentum*

endo-beta-1,4-D-glucanase. Cel8.

---

BAA94257.1 AB040769 *Hordeum vulgare*

endo-1,4-beta-glucanase Cel1. Cel1.

---

AAC49704.1 U78526 *Lycopersicon esculentum*

endo-1,4-beta-glucanase. Cel3.

---

CAB51903.1 AJ242807 *Brassica napus*

endo-1,4-beta-D-glucanase. Cell16. cellulase.

---

AAA20082.1 U00730 *Glycine max*

CMCase; cellulase; endo-1,4-beta-D-glucanase.

---

CAA11301.1 AJ223386 *Fragaria x ananassa*

endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by RT-PCR amplification.

---

CAA11302.1 AJ223387 *Fragaria x ananassa*

endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR amplification.

---

BAA21111.1 D88417 *Gossypium hirsutum*

endo-1,4-beta-glucanase.

---

AAA20083.1 U00731 *Glycine max*

CMCase; cellulase; endo-1,4-beta-D-glucanase.

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SEQ ID NO: 560

AAB97617.1 U83687 *Apium graveolens*

NADPH-dependent mannose 6-phosphate reductase. m6pr. aldo-keto reductase; similar to aldose 6-phosphate reductase also known as NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession Number D11080.

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AAC97607.1 AF057134 *Malus x domestica*

synthesizes sorbitol, a major photosynthetic product in many members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate dehydrogenase. S6PDH.

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BAA01853.1 D11080 *Malus x domestica*

NADP-dependent D-sorbitol-6-phosphate dehydrogenase. S6PDH.

---

SEQ ID NO: 561

CAB43938.1 AJ006349 *Fragaria x ananassa*

cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.

---

BAA96209.1 AP002094 *Oryza sativa*

EST C72268(E1328) corresponds to a region of the predicted gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).

---

BAA96207.1 AP002094 *Oryza sativa*

EST C72268(E1328) corresponds to a region of the predicted gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).

---

AAD08699.1 AF098292 *Lycopersicon esculentum*  
endo-beta-1,4-D-glucanase. Cel8.

BAA21111.1 D88417 *Gossypium hirsutum*  
endo-1,4-beta-glucanase.

CAA65828.1 X97190 *Capsicum annuum*  
endo-beta-1,4-glucanase. ccel2.

CAB59900.1 AJ010950 *Capsicum annuum*  
cell wall degradation. endo-beta-1,4-glucanase. eg2.

AAC95009.1 AF074923 *Fragaria x ananassa*  
endo-1,4-beta-glucanase precursor. Cel1. 1,4-beta-glucanohydrolase.

CAB43937.1 AJ006348 *Fragaria x ananassa*  
cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.

AAA80495.1 U20590 *Lycopersicon esculentum*  
endo-1,4-beta-glucanase precursor. cellulase.

BAA85150.1 AB032830 *Pisum sativum*  
endo-1,4-beta-glucanase. EGL2.

AAC12684.1 U76725 *Pinus radiata*  
endo-beta-1,4-glucanase. PrCell1. cellulase; PRCEL1.

BAB32662.1 AB055886 *Atriplex lentiformis*  
beta-1,4-glucanase. Al-cell1. cellulase.

AAC62241.1 AF077339 *Lycopersicon esculentum*  
endo-1,4-beta-glucanase. cel5. cellulase; also expressed in fruit and pistils.

CAA65826.1 X97188 *Capsicum annuum*  
endo-beta-1,4-glucanase. ccel1. cellulase.

AAA69909.1 U13055 *Lycopersicon esculentum*  
cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel2. cellulase.

CAA65597.1 X96853 *Prunus persica*  
endo-beta-1,4-glucanase. pcell1.

CAA65600.1 X96856 *Prunus persica*  
endo-beta-1,4-glucanase. ppEG1.

AAC12685.1 U76756 *Pinus radiata*  
endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.

BAB39482.1 AB049199 *Populus alba*  
endo-1,4-beta glucanase. PopCell1.

CAA65827.1 X97189 *Capsicum annuum*  
endo-beta-1,4-glucanase. ccel3. cellulase.

BAB39483.1 AB049200 *Populus alba*  
endo-1,4-beta-glucanase. PopCel2.

BAA77239.1 AB025796 *Populus alba*  
endo-1,4-beta glucanase. POPCEL2. cellulase.

AAA69908.1 U13054 *Lycopersicon esculentum*  
cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel1. cellulase.

AAC78504.1	U34754	Phaseolus vulgaris endo-1,4-beta-D-glucanase. cellulase.
AAA02563.1	M57400	Phaseolus vulgaris cellulase precursor. endo-1,4-beta-D-glucanase.
CAA72133.1	Y11268	Lycopersicon esculentum endo-1,4-beta-D-glucanase. cel7.
AAC96135.1	L41046	Pisum sativum endo-1,4-beta-glucanase. EGL1.
CAB51903.1	AJ242807	Brassica napus endo-1,4-beta-D-glucanase. Cel16. cellulase.
AAC49704.1	U78526	Lycopersicon esculentum endo-1,4-beta-glucanase. Cel3.
BAA94257.1	AB040769	Hordeum vulgare endo-1,4-beta-glucanase Cell. Cell1.
CAA11302.1	AJ223387	Fragaria x ananassa endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR amplification.
AAA20082.1	U00730	Glycine max CMCase; cellulase; endo-1,4-beta-D-glucanase.
CAA11301.1	AJ223386	Fragaria x ananassa endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by RT-PCR amplification.
AAC64045.1	AF077340	Lycopersicon esculentum endo-1,4-beta-glucanase. cel5. cellulase.
SEQ ID NO: 562		
AAD53011.1	AF089848	Brassica napus senescence-specific cysteine protease. SAG12-1. BnSAG12-1.
AAD53012.1	AF089849	Brassica napus senescence-specific cysteine protease. SAG12-2. BnSAG12-2.
AAK27968.1	AF242372	Ipomoea batatas cysteine protease. SPCP1.
AAA50755.1	U13940	Alnus glutinosa cysteine proteinase. putative preprotein.
BAB13759.1	AB040454	Astragalus sinicus cysteine proteinase. AsNODf32. preprotein putative.
AAC62396.1	AF050756	Ricinus communis cysteine endopeptidase precursor. CysEP.
CAB09698.1	Z97022	Hordeum vulgare cysteine proteinase. putative.
CAA52425.1	X74406	Hemerocallis sp. thiol-protease. SEN102.
BAA83472.1	AB004648	Oryza sativa cysteine endopeptidase. RepA.

CAA56844.1 X80876 *Oryza sativa*  
cysteine protease.

BAA88898.1 AB020961 *Zea mays*  
cysteine protease component of protease-inhibitor complex. CPPIC.

AAC35211.1 U12637 *Hemerocallis* hybrid cultivar  
cysteine proteinase. SEN11.

CAB09697.1 Z97021 *Hordeum vulgare*  
cysteine endopeptidase EP-A. precursor.

AAB88263.1 AF019147 *Zea mays*  
cysteine proteinase Mir3. mir3.

AAD28477.1 AF133839 *Sandersonia aurantiaca*  
papain-like cysteine protease. PRT5. senescence-related.

CAB16317.1 Z99173 *Nicotiana tabacum*  
storage protein hydrolysis. cysteine proteinase precursor.

CAB09699.1 Z97023 *Hordeum vulgare*  
cysteine endopeptidase EP-A.

AAD10337.1 U94591 *Hordeum vulgare*  
cysteine proteinase precursor. EPA.

CAA06243.1 AJ004958 *Pisum sativum*  
thiol-protease. pre-pro-TPE4A protein. tpE4A.

CAB53515.1 AJ245924 *Solanum tuberosum*  
proteolysis. cysteine protease. cyp.

AAD48496.1 AF172856 *Lycopersicon esculentum*  
cysteine protease TDI-65. tdi-65. induced by drought; localized in the nuclei and chloroplast  
(Tabaeizadeh, Z. et al., 1995. *Protoplasma*, 186:208-219).

CAA05894.1 AJ003137 *Lycopersicon esculentum*  
cysteine protease. CYP1. C14.

AAA79915.1 U17135 *Dianthus caryophyllus*  
cysteine proteinase. DCCP1. expressed in senescing flower petals.

AAB37233.1 U34747 *Phalaenopsis* sp. SM9108  
cysteine proteinase.

CAB17076.1 Z99954 *Phaseolus vulgaris*  
protein hydrolysis. cysteine proteinase precursor.

CAA84378.1 Z34895 *Vicia sativa*  
storage protein degradation. cysteine proteinase.

CAA53377.1 X75749 *Vicia sativa*  
storage protein hydrolysis. cysteine protease.

CAB17074.1 Z99952 *Phaseolus vulgaris*  
degradation of storage proteins. cysteine proteinase precursor.

AAB68374.1 U52970 *Phaseolus vulgaris*  
suggested to initiate phaseolin degradation during germination. cysteine endopeptidase 1.  
PvCEP-1.

CAA12118.1 AJ224766 Phaseolus vulgaris  
phaseolin degradation. cysteine protease.

AAC49455.1 U41902 Pseudotsuga menziesii  
cysteine protease. Pseudotzain. PM33cysP.

CAA46863.1 X66061 Pisum sativum  
thiolprotease. tpp. start codon ttg.

AAB41816.1 U44947 Pisum sativum  
NTH1. PsCyp1. cysteine protease homolog.

BAA83473.1 AB004819 Oryza sativa  
cysteine endopeptidase. Rep1.

BAA22544.1 D38532 Ananas comosus  
precursor of cysteine proteinase. FBSB precursor. stem bromelain precursor in fruit.

BAA11170.1 D76415 Oryza sativa  
cysteine proteinase.

AAD20453.1 AF099203 Oryza sativa  
cysteine endopeptidase precursor. EP3A.

CAA08860.1 AJ009829 Ananas comosus  
cysteine proteinase precursor, AN8. an8.

AAA85036.1 U19384 Hordeum vulgare  
cysteine proteinase EPB2 precursor.

AAA85035.1 U19359 Hordeum vulgare  
cysteine proteinase EPB1 precursor.

SEQ ID NO: 565

AAA97411.1 U51918 Pisum sativum  
pyruvate dehydrogenase E1 alpha subunit.

CAA81558.1 Z26949 Solanum tuberosum  
subunit of the mitochondrial pyruvate dehydrogenase complex. E1 alpha subunit of pyruvate dehydrogenase precursor.

AAC72195.1 AF069911 Zea mays  
pyruvate dehydrogenase E1 alpha subunit.

AAG43499.1 AF209924 Lycopersicon esculentum  
pyruvate dehydrogenase.

CAB08111.1 Z941S0 Lycopersicon esculentum  
branched chain alpha-keto acid dehydrogenase E1-alpha subunit.

SEQ ID NO: 566

AAD55090.1 AF178653 Vitis riparia  
thaumatin. osmotin; pathogenesis-related protein.

CAA51432.1 X72928 Solanum commersonii  
osmotin-like protein.

CAA47601.1 X67121 Solanum commersonii  
osmotin-like protein.

CAC34055.1 AJ297410 Capsicum annuum  
osmotin-like protein. pr5 p23.

CAA47047.1 X66416 *Lycopersicon esculentum*  
tpm 1. Induced during viroid infection. Osmotin-like, antifungal protein homologue.

AAB23375.1 S44889 *Nicotiana tabacum*  
osmotin. osmotin. pathogenesis-related protein homolog; This sequence comes from Fig. 3.

AAB22459.2 S40046 *Nicotiana tabacum*  
osmotin. abscisic acid-activated. basic PR-like protein; This sequence comes from Fig. 1A; conceptual translation presented here differs from translation in publication; mismatch(181[R->G]).

AAG16625.1 AY007309 *Solanum dulcamara*  
cryoprotective osmotin-like protein.

CAA46623.1 X65701 *Nicotiana tabacum*  
osmotin. AP24.

CAA46622.1 X65700 *Nicotiana tabacum*  
osmotin. AP24.

CAA51431.1 X72927 *Solanum commersonii*  
osmotin-like protein.

CAA64620.1 X95308 *Nicotiana tabacum*  
PR protein. osmotin.

CAA51430.1 X72926 *Solanum commersonii*  
osmotin-like protein.

AAC64171.1 AF093743 *Lycopersicon esculentum*  
pathogenesis-related protein osmotin precursor. NP24.

AAB61590.1 AF003007 *Vitis vinifera*  
VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.

BAA11180.1 D76437 *Nicotiana sylvestris*  
antifungal activity. neutral PR-5 (osmotin-like protein, PR-5d). neutral isoform of pathogenesis-related protein group 5.

AAA34087.1 M64081 *Nicotiana tabacum*  
osmotin-like protein. OLP1.

CAA47669.1 X67244 *Solanum commersonii*  
osmotin-like protein.

CAA71883.1 Y10992 *Vitis vinifera*  
osmotin-like protein. OSM1.

AAF13707.1 AF199508 *Fragaria x ananassa*  
osmotin-like protein. olp.

AAA34089.1 M29279 *Nicotiana tabacum*  
osmotin.

CAA43854.1 X61679 *Nicotiana tabacum*  
osmotin.

CAA04642.1 AJ001268 *Hordeum vulgare*  
antifungal. basic pathogenesis-related protein PR5. osmotin/permatin-like.

CAC22330.1 AJ298304 *Fagus sylvatica*  
stress protein. osmotin-like protein. olp2.

CAC22329.1 AJ298303 *Fagus sylvatica*  
stress protein. osmotin-like protein. olp.

AAB67852.1 L76377 *Oryza sativa*  
osmotin. 14b.

CAB36911.1 AJ000692 *Quercus suber*  
stress protein. osmotin-like protein. olp.

SEQ ID NO: 569

BAA95814.1 AP002069 *Oryza sativa*

ESTs AU082579(S2069),D40238(S2069) correspond to a region of the predicted gene.  
Similar to *Arabidopsis thaliana* vesicle-associated membrane protein 7C; synaptobrevin 7C.  
(AF025332).

SEQ ID NO: 572

AAA92677.1 U13736 *Pisum sativum*  
binds calcium. calmodulin-like protein.

AAA34015.1 L01433 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-4. putative.

AAA33948.1 L19359 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-5. putative.

CAA66159.1 X97558 *Capsicum annuum*  
calmodulin-1.

CAA09302.1 AJ010645 *Capsicum annuum*  
calcium binding protein. calmodulin 3 protein. calmodulin 3.

AAA34144.1 M67472 *Lycopersicon esculentum*  
calmodulin. CALM1LE.

CAA62150.1 X90560 *Physcomitrella patens*  
Calmodulin. CaM.

AAB46588.1 U83402 *Capsicum annuum*  
calmodulin.

BAA87825.1 AP000815 *Oryza sativa*  
ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene.  
Similar to *O.sativa* gene encoding calmodulin. (Z12828).

AAF65511.1 AF108889 *Capsicum annuum*  
calmodulin.

AAA85157.1 U20297 *Solanum tuberosum*  
calcium-binding protein. calmodulin.

AAA85156.1 U20296 *Solanum tuberosum*  
calcium-binding protein. calmodulin.

AAA62351.1 U20295 *Solanum tuberosum*  
calcium-binding protein. calmodulin.

AAA85155.1 U20294 *Solanum tuberosum*  
calcium-binding protein. calmodulin.

AAA33900.1 L18914 *Oryza sativa*  
calcium binding protein, signal transduction. calmodulin.

CAA78288.1	Z12828	Oryza sativa calcium binding protein, signal transduction. calmodulin.
AAC49583.1	U48692	Triticum aestivum calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum calmodulin TaCaM2-2. calcium-binding protein.
CAA61980.1	X89890	Bidens pilosa Calmodulin.
CAA67054.1	X98404	Capsicum annuum calmodulin-2.
AAA33083.1	M20729	Chlamydomonas reinhardtii calmodulin.
AAG11418.1	AF292108	Prunus avium calmodulin.
AAF33852.1	AF231026	Oryza sativa calmodulin-like protein.
AAA92681.1	U13882	Pisum sativum calcium-binding protein. calmodulin.
AAA33706.1	M80836	Petunia x hybrida calmodulin. CAM81.
AAA33705.1	M80831	Petunia x hybrida calmodulin-related protein. CAM53.
AAA98933.1	U37936	Oryza sativa novel calmodulin-like protein. C-terminal of this sequence contains a CAAX box which is common in signal transport protein, but not in calmodulin.
CAA43143.1	X60738	Malus x domestica Calmodulin. CaM.
CAA78301.1	Z12839	Lilium longiflorum calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum calcium binding protein, signal transduction. calmodulin. putative.
CAA42423.1	X59751	Daucus carota calmodulin. Ccam-1.
AAFF73157.1	AF150059	Brassica napus calmodulin. CaM1. involved in seed germination.
AAA19571.1	U10150	Brassica napus calcium binding. calmodulin. bcm1.
AAA87347.1	M88307	Brassica juncea calmodulin.
AAG27432.1	AF295637	Elaeis guineensis calmodulin.
BAA94697.1	AB041712	Chara corallina calmodulin. cccam2.

BAA94696.1 AB041711 Chara corallina  
calmodulin. cccam1.

BAA96536.1 AB044286 Chara corallina  
calmodulin. ccam.

AAC18355.1 AF064456 Oryza sativa subsp. indica  
calmodulin-like protein. CAM-like.

AAA34237.1 L20691 Vigna radiata  
calmodulin.

CAA52602.1 X74490 Zea mays  
Calmodulin. ZMCALM1.

CAA54583.1 X77397 Zea mays  
calmodulin. CaM2.

AAC49585.1 U49103 Triticum aestivum  
calmodulin TaCaM3-2. calcium-binding protein.

AAC49586.1 U49104 Triticum aestivum  
calmodulin TaCaM3-3. calcium-binding protein.

AAC49587.1 U49105 Triticum aestivum  
calmodulin TaCaM4-1. calcium-binding protein.

AAC49580.1 U48689 Triticum aestivum  
calmodulin TaCaM1-3. calcium-binding protein.

AAC49584.1 U48693 Triticum aestivum  
calmodulin TaCaM3-1. calcium-binding protein.

SEQ ID NO: 575

AAK28303.1 AF346431 Nicotiana tabacum  
phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.

AAB36653.1 U32644 Nicotiana tabacum  
immediate-early salicylate-induced glucosyltransferase. IS5a.

AAB36652.1 U32643 Nicotiana tabacum  
immediate-early salicylate-induced glucosyltransferase. IS10a.

AAK28304.1 AF346432 Nicotiana tabacum  
phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.

CAA59450.1 X85138 Lycopersicon esculentum  
tw1. homologous to glucosyltransferases.

CAB56231.1 Y18871 Dorotheanthus bellidiformis  
betanidin-5-O-glucosyltransferase.

BAA83484.1 AB031274 Scutellaria baicalensis  
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

AAB48444.1 U82367 Solanum tuberosum  
UDP-glucose glucosyltransferase.

CAA54610.1 X77460 Manihot esculenta  
UTP-glucose glucosyltransferase. CGT4.

AAD04166.1 AF101972 *Phaseolus lunatus*  
catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

BAB17182.1 AP002843 *Oryza sativa*  
putative UTP-glucose glucosyltransferase. P0407B12.19.

BAA93039.1 AB033758 *Citrus unshiu*  
limonoid UDP-glucosyltransferase. LGTase.

AAF61647.1 AF190634 *Nicotiana tabacum*  
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAB17176.1 AP002843 *Oryza sativa*  
putative UTP-glucose glucosyltransferase. P0407B12.13.

CAC09351.1 AL442007 *Oryza sativa*  
putative glucosyltransferase. H0212B02.7.

CAA54611.1 X77461 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT2.

AAF98390.1 AF287143 *Brassica napus*  
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

AAK16181.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.16.

AAK16178.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.5.

CAA54612.1 X77462 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT5.

AAK16180.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.21.

AAF17077.1 AF199453 *Sorghum bicolor*  
UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.

CAA54609.1 X77459 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT1.

BAB41025.1 AB047098 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. FlUFGT1.

AAK16172.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.14.

BAB41019.1 AB047092 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.

BAB41018.1 AB047091 *Vitis labrusca x Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.

BAB41023.1 AB047096 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. *AlUFGT1*.

BAB41021.1 AB047094 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. *RuUFGT1*.

BAA89009.1 AB027455 *Petunia x hybrida*  
anthocyanin 5-O-glucosyltransferase. *PH1*.

AAB81682.1 AF000371 *Vitis vinifera*  
UDP glucose:flavonoid 3-o-glucosyltransferase.

BAB41017.1 AB047090 *Vitis labrusca x Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. *KyUFGT1*. The gene was derived from one of the parents *V. labruscana* cv. *Ishiharawase*.

BAB41022.1 AB047095 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. *RuUFGT2*.

BAB41020.1 AB047093 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. *ItUFGT2*.

BAB41024.1 AB047097 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. *AlUFGT2*.

AAB81683.1 AF000372 *Vitis vinifera*  
UDP glucose:flavonoid 3-o-glucosyltransferase.

BAB41026.1 AB047099 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. *FlUFGT2*.

CAA54613.1 X77463 *Manihot esculenta*  
UTP-glucose glucosyltransferase. *CGT6*.

BAA89008.1 AB027454 *Petunia x hybrida*  
anthocyanin 3-O-glucosyltransferase. *PGT8*.

BAA12737.1 D85186 *Gentiana triflora*  
UDP-glucose:flavonoid-3-glucosyltransferase.

SEQ ID NO: 576

CAB60277.1 AJ002586 *Solanum tuberosum*  
UCP.

CAA72107.1 Y11220 *Solanum tuberosum*  
mitochondrial uncoupling protein.

BAA92172.1 AB024733 *Symplocarpus renifolius*  
SfUCPa. SfUCPa.

BAB40658.1 AB049998 *Oryza sativa*  
uncoupling protein. *OsUCP2*.

BAA92173.1 AB024734 *Symplocarpus renifolius*  
SfUCPb. SfUCPb.

BAB16385.1 AB042429 *Triticum aestivum*  
uncoupling protein. *WhUCP1b*.

BAB16384.1 AB042428 *Triticum aestivum*  
uncoupling protein. *WhUCP1a*.

BAB40657.1 AB049997 *Oryza sativa*  
uncoupling protein. OsUCP1.

SEQ ID NO: 577

AAA19571.1 U10150 *Brassica napus*  
calcium binding. calmodulin. bcm1.

AAA87347.1 M88307 *Brassica juncea*  
calmodulin.

AAA92681.1 U13882 *Pisum sativum*  
calcium-binding protein. calmodulin.

AAA33706.1 M80836 *Petunia x hybrida*  
calmodulin. CAM81.

CAA43143.1 X60738 *Malus x domestica*  
Calmodulin. CaM.

CAA78301.1 Z12839 *Lilium longiflorum*  
calcium binding protein, signal transduction. calmodulin.

AAA33397.1 L18912 *Lilium longiflorum*  
calcium binding protein, signal transduction. calmodulin. putative.

CAA42423.1 X59751 *Daucus carota*  
calmodulin. Ccam-1.

AAG27432.1 AF295637 *Elaeis guineensis*  
calmodulin.

AAG11418.1 AF292108 *Prunus avium*  
calmodulin.

AAA34237.1 L20691 *Vigna radiata*  
calmodulin.

AAC49587.1 U49105 *Triticum aestivum*  
calmodulin TaCaM4-1. calcium-binding protein.

AAC49586.1 U49104 *Triticum aestivum*  
calmodulin TaCaM3-3. calcium-binding protein.

AAC49585.1 U49103 *Triticum aestivum*  
calmodulin TaCaM3-2. calcium-binding protein.

AAC49584.1 U48693 *Triticum aestivum*  
calmodulin TaCaM3-1. calcium-binding protein.

AAC49580.1 U48689 *Triticum aestivum*  
calmodulin TaCaM1-3. calcium-binding protein.

AAC49579.1 U48688 *Triticum aestivum*  
calmodulin TaCaM1-2. calcium binding protein.

AAC49578.1 U48242 *Triticum aestivum*  
calmodulin TaCaM1-1. calcium-binding.

AAA03580.1 L01431 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-2. putative.

AAB36130.1 S81594 *Vigna radiata*  
auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from  
Fig. 1; arCaM.

AAA33901.1 L18913 *Oryza sativa*  
calcium binding protein, signal transduction. calmodulin. putative.

CAA78287.1 Z12827 *Oryza sativa*  
calcium binding protein, signal transduction. calmodulin.

AAB46588.1 U83402 *Capsicum annuum*  
calmodulin.

AAA32938.1 M27303 *Hordeum vulgare*  
calmodulin.

BAA88540.1 AP000969 *Oryza sativa*  
ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene.  
Similar to calmodulin. (AF042840).

AAF65511.1 AF108889 *Capsicum annuum*  
calmodulin.

AAC36059.1 AF042840 *Oryza sativa*  
calmodulin. CaM1.

AAA34238.1 L20507 *Vigna radiata*  
calmodulin.

AAA34014.1 L01432 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-3. putative.

AAA34013.1 L01430 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-1. putative.

CAA36644.1 X52398 *Medicago sativa*  
calmodulin (AA 1-149).

AAB68399.1 U79736 *Helianthus annuus*  
calmodulin. HaCaM.

AAD10244.1 AF030032 *Phaseolus vulgaris*  
calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal  
transduction pathways.

AAA33705.1 M80831 *Petunia x hybrida*  
calmodulin-related protein. CAM53.

AAA16320.1 L14071 *Bryonia dioica*  
calmodulin. Bc329. calcium-binding sites (amino acid #): 1. (21..33); 2. (57..68); 3. (94..106);  
4. (130..141).

CAA61980.1 X89890 *Bidens pilosa*  
Calmodulin.

AAA33900.1 L18914 *Oryza sativa*  
calcium binding protein, signal transduction. calmodulin.

CAA78288.1 Z12828 *Oryza sativa*  
calcium binding protein, signal transduction. calmodulin.

CAA74307.1	Y13974	Zea mays calmodulin.
AAC49583.1	U48692	Triticum aestivum calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum calmodulin TaCaM2-2. calcium-binding protein.
AAA85157.1	U20297	Solanum tuberosum calcium-binding protein. calmodulin.
AAA85156.1	U20296	Solanum tuberosum calcium-binding protein. calmodulin.
AAA62351.1	U20295	Solanum tuberosum calcium-binding protein. calmodulin.
AAA85155.1	U20294	Solanum tuberosum calcium-binding protein. calmodulin.
CAA46150.1	X65016	Oryza sativa calmodulin. cam.
AAD10246.1	AF030034	Phaseolus vulgaris calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
AAF73157.1	AF150059	Brassica napus calmodulin. CaM1. involved in seed germination.
CAA54583.1	X77397	Zea mays calmodulin. CaM2.
SEQ ID NO: 578		
AAF01764.2	AF184277	Glycine max homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
BAA21017.1	D26578	Daucus carota transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.
AAD37697.1	AF145728	Oryza sativa homeodomain leucine zipper protein. Oshox4. transcription factor.
CAB67118.1	Y17306	Lycopersicon esculentum homeodomain protein. h52.
AAF01765.1	AF184278	Glycine max homeodomain-leucine zipper protein 57. Hdl57. transcription factor.
BAA05624.1	D26575	Daucus carota transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.
BAA93466.1	AB028078	Physcomitrella patens homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.
BAA93465.1	AB028077	Physcomitrella patens homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.

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BAA93464.1 AB028076 *Physcomitrella patens*  
homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.

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BAA05622.1 D26573 *Daucus carota*  
transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.

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BAA05625.1 D26576 *Daucus carota*  
transcriptional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.

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BAA05623.1 D26574 *Daucus carota*  
transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.

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AAD37698.1 AF145729 *Oryza sativa*  
homeodomain leucine zipper protein. Oshox5. transcription factor.

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BAA93461.1 AB028073 *Physcomitrella patens*  
homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.

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BAA93467.1 AB028079 *Physcomitrella patens*  
homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.

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BAA93468.1 AB028080 *Physcomitrella patens*  
homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.

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BAA93460.1 AB028072 *Physcomitrella patens*  
homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.

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AAD37699.1 AF145730 *Oryza sativa*  
homeodomain leucine zipper protein. Oshox6. transcription factor.

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CAA06717.1 AJ005820 *Craterostigma plantagineum*  
transcription factor. homeodomain leucine zipper protein. hb-1.

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BAA93463.1 AB028075 *Physcomitrella patens*  
homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.

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CAA65456.2 X96681 *Oryza sativa*  
transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.

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AAF19980.1 AF211193 *Oryza sativa*  
homeodomain-leucine zipper transcription factor. Hox1. hox1.

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AAK31270.1 AC079890 *Oryza sativa*  
homeodomain leucine zipper protein hox1. OSJNBb0089A17.12.

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CAA06728.1 AJ005833 *Craterostigma plantagineum*  
transcription factor. homeodomain leucine zipper protein. hb-2.

---

AAD37696.1 AF145727 *Oryza sativa*  
homeodomain leucine zipper protein. Oshox3. transcription factor.

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SEQ ID NO: 580

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AAD32141.1 AF123503 *Nicotiana tabacum*  
Nt-gh3 deduced protein.

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CAA42636.1 X60033 *Glycine max*  
auxin-responsive GH3 product. GH3.

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BAA96221.1 AP002094 *Oryza sativa*

ESTs C19814(E10971),AU090481(E10971) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, sequence from clones T3F17, F11C10, F13A10; auxin-responsive GH3-like protein (AC006526).

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SEQ ID NO: 581

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AAD13632.1 AF059488 *Lycopersicon esculentum*  
expansin precursor. Exp4.

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AAF32410.1 AF230277 *Triphysaria versicolor*  
alpha-expansin 2.

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CAA04385.1 AJ000885 *Brassica napus*  
Cell wall extension in plants. Expansin.

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CAB46492.1 AJ243340 *Lycopersicon esculentum*  
expansin9. exp9.

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AAC63088.1 U82123 *Lycopersicon esculentum*  
expansin. LeEXP1. fruit ripening regulated expansin.

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CAA06271.2 AJ004997 *Lycopersicon esculentum*  
expansin18. exp18.

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AAF62182.1 AF247164 *Oryza sativa*  
alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.

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AAF35900.1 AF230331 *Zinnia elegans*  
expansin. Exp1.

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AAG13982.1 AF297521 *Prunus avium*  
expansin 1. Exp1. PruavExp1.

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AAC33529.1 U93167 *Prunus armeniaca*  
expansin. PA-Exp1.

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AAF21101.1 AF159563 *Fragaria x ananassa*  
expansin. Exp2. ripening regulated.

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AAF35901.1 AF230332 *Zinnia elegans*  
expansin 2.

---

AAG13983.1 AF297522 *Prunus avium*  
expansin 2. Exp2. PruavExp2.

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AAC33530.1 AF038815 *Prunus armeniaca*  
expansin. Exp2.

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BAB19676.1 AB029083 *Prunus persica*  
expansin. PchExp1.

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AAB40637.1 U64893 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

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AAB37746.1 U30382 *Cucumis sativus*  
expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.

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CAC19184.1 AJ291817 *Cicer arietinum*  
expansin.

AAD47901.1 AF085330 *Pinus taeda*  
expansin.

AAB40634.1 U64890 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAF32409.1 AF230276 *Triphysaria versicolor*  
alpha-expansin 3.

AAC39512.1 AF043284 *Gossypium hirsutum*  
expansin. GhEX1. contains N-terminal signal peptide.

AAB40635.1 U64891 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAC96081.1 AF049354 *Nicotiana tabacum*  
involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.

AAB38074.1 U30477 *Oryza sativa*  
induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.

AAG32921.1 AF184233 *Lycopersicon esculentum*  
expansin. Exp10.

AAB81662.1 U85246 *Oryza sativa*  
expansin. Os-EXP4.

AAD49956.1 AF167360 *Rumex palustris*  
expansin. EXP1.

AAB40636.1 U64892 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAF32411.1 AF230278 *Triphysaria versicolor*  
alpha-expansin 1.

AAC96080.1 AF049353 *Nicotiana tabacum*  
involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.

AAF35902.1 AF230333 *Zinnia elegans*  
expansin 3.

CAB43197.1 AJ239068 *Lycopersicon esculentum*  
cell wall loosening enzyme. expansin2. exp2.

AAC64201.1 AF096776 *Lycopersicon esculentum*  
expansin. LeEXP2.

AAF17570.1	AF202119	Marsilea quadrifolia alpha-expansin. EXP1. Mq-EXP1.
AAD13633.1	AF059489	Lycopersicon esculentum expansin precursor. Exp5.
AAF62181.1	AF247163	Oryza sativa alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAF17571.1	AF202120	Regnellidium diphyllum alpha-expansin. EXP1. Rd-EXP1.
AAF62180.1	AF247162	Oryza sativa alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
CAC19183.1	AJ291816	Cicer arietinum expansin.
CAC06433.1	AJ276007	Festuca pratensis expansin. exp2.
BAB32732.1	AB049406	Eustoma grandiflorum expansin. Eg Expansin.
AAG01875.1	AF291659	Striga asiatica alpha-expansin 3. Exp3.
AAB37749.1	U30460	Cucumis sativus expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAC96077.1	AF049350	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAC96079.1	AF049352	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
AAG32920.1	AF184232	Lycopersicon esculentum expansin. Exp8.
CAA69105.1	Y07782	Oryza sativa expansin. RiExA.
AAC96078.1	AF049351	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
SEQ ID NO: 583		
BAA85412.1	AP000615	Oryza sativa ESTs AU065232(E60855), C23624(S1554), AU078241(E60855) correspond to a region of the predicted gene.; similar to putative adenylate kinase. (AC005896).
BAA01181.1	D10335	Oryza sativa adenylate kinase-b. Adk-b.
BAA01180.1	D10334	Oryza sativa adenylate kinase-a. Adk-a.
BAA94761.1	AB041773	Oryza sativa adenylate kinase. Adk-a.

AAB68604.1 U82330 *Prunus armeniaca*  
adenylate kinase homolog.

AAF23372.1 AF187063 *Oryza sativa*  
catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase b. ura6.

AAF23371.1 AF187062 *Oryza sativa*  
catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase a. ura6.

AAD41679.1 AF086603 *Ceratopteris richardii*  
adenylate kinase. ADK1.

BAA85443.1 AP000616 *Oryza sativa*  
similar to UMP/CMP kinase (AF000147).

SEQ ID NO: 584

BAA87052.2 D88273 *Hordeum vulgare*  
nicotianamine aminotransferase A. naat-A.

BAA87055.1 AB024006 *Hordeum vulgare*  
nicotianamine aminotransferase. naat-A.

BAA87053.1 AB005788 *Hordeum vulgare*  
nicotianamine aminotransferase B. naat-b. NAAT-B.

BAA87054.1 AB024006 *Hordeum vulgare*  
nicotianamine aminotransferase. naat-B.

BAA77261.1 AB007405 *Oryza sativa*  
alanine aminotransferase. AlaAT.

BAA77260.1 AB007404 *Oryza sativa*  
alanine aminotransferase. AlaAT.

CAA49199.1 X69421 *Panicum miliaceum*  
alanine aminotransferase. pAlaAT-2.

AAB01685.1 U31975 *Chlamydomonas reinhardtii*  
catalyzes the transfer of -NH2 from ala to 2-oxoglutarate. alanine aminotransferase. The translation start site has not been experimentally tested, but a 55 kDa product can be detected in Western blot.

AAC62456.1 AF055898 *Zea mays*  
alanine aminotransferase. alt. AlaAT.

CAA81231.1 Z26322 *Hordeum vulgare*  
alanine aminotransferase.

SEQ ID NO: 586

AAB94589.1 AF022460 *Glycine max*  
CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.

AAA32913.1 M32885 *Persea americana*  
cytochrome P-450LXXIA1 (cyp71A1).

AAA19701.1 L24438 *Thlaspi arvense*  
cytochrome P450.

BAB40324.1 AB037245 *Asparagus officinalis*  
cytochrome P450. ASPI-2.

AAC39318.1 AF029858 *Sorghum bicolor*  
second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic  
glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-  
hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.

BAB40323.1 AB037244 *Asparagus officinalis*  
cytochrome P450. ASPI-1.

CAA71517.1 Y10493 *Glycine max*  
putative cytochrome P450.

AAB61965.1 U48435 *Solanum chacoense*  
putative cytochrome P450.

CAA70575.1 Y09423 *Nepeta racemosa*  
cytochrome P450. CYP71A5.

CAA71513.1 Y10489 *Glycine max*  
putative cytochrome P450.

AAB61964.1 U48434 *Solanum chacoense*  
putative cytochrome P450.

AAD47832.1 AF166332 *Nicotiana tabacum*  
cytochrome P450.

AAB94588.1 AF022459 *Glycine max*  
CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

AAF27282.1 AF122821 *Capsicum annuum*  
cytochrome P450. PepCYP.

CAA50312.1 X70981 *Solanum melongena*  
P450 hydroxylase. CYPEG2.

CAA83941.1 Z33875 *Mentha x piperita*  
cytochrome P-450 oxidase.

AAG44132.1 AF218296 *Pisum sativum*  
cytochrome P450. P450 isolog.

CAA70576.1 Y09424 *Nepeta racemosa*  
cytochrome P450. CYP71A6.

AAD44151.1 AF124816 *Mentha x piperita*  
cytochrome p450 isoform PM17.

BAA03635.1 D14990 *Solanum melongena*  
Cytochrome P-450EG4.

CAA50645.1 X71654 *Solanum melongena*  
P450 hydroxylase.

AAB69644.1 AF000403 *Lotus japonicus*  
putative cytochrome P450. LjNP450.

AAD37433.1 AF150881 *Lycopersicon esculentum x Lycopersicon peruvianum*  
catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase.  
CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.

CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.
AAD44152.1	AF124817	Mentha x piperita cytochrome p450 isoform PM2.
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
AAG14962.1	AF214008	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H2.
AAG14961.1	AF214007	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H1.
CAB56503.1	AJ238612	Catharanthus roseus cytochrome P450.
AAG14963.1	AF214009	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H3.
AAK38088.1	AF321864	Lolium rigidum putative cytochrome P450.
AAD44150.1	AF124815	Mentha spicata cytochrome p450.
AAK38084.1	AF321860	Lolium rigidum putative cytochrome P450.
AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAK38087.1	AF321863	Lolium rigidum putative cytochrome P450.
AAK38083.1	AF321859	Lolium rigidum putative cytochrome P450.
AAB94584.1	AF022157	Glycine max capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
CAA71514.1	Y10490	Glycine max putative cytochrome P450.
BAA12159.1	D83968	Glycine max Cytochrome P-450 (CYP93A1).
BAB39252.1	AP002968	Oryza sativa putative cytochrome P450. P0416G11.1.
CAA50155.1	X70824	Solanum melongena flavonoid hydroxylase (P450). CYP75.
SEQ ID NO: 587		
CAA60120.1	X86222	Pisum sativum heat shock protein. hsp22.
AAF37726.1	AF237957	Euphorbia esula LMW heat shock protein. putative 22 kDa mitochondrial heat shock protein.

BAA32547.1 AB017134 *Lycopersicon esculentum*  
mitochondrial small heat shock protein. LEMTSHP.

CAA33388.1 X15333 *Chenopodium rubrum*  
heat shock protein (AA 1-204).

AAB03096.1 U21722 *Glycine max*  
Hsp23.9. Gmhsp23.9. low molecular weight heat shock protein.

AAC12279.1 AF035460 *Zea mays*  
low molecular weight heat shock protein precursor. hsp22.

AAD03604.1 AF104107 *Triticum aestivum*  
small heat shock protein Hsp23.5. mRNA not present, or only at very low levels, prior to heat stress; mRNA abundant after two hours at 40C.

AAB01557.1 L47741 *Picea glauca*  
mitochondria-localized low molecular weight heat shock protein 23.5. EMB22, SMW HSP23.5.

AAD03605.1 AF104108 *Triticum aestivum*  
small heat shock protein Hsp23.6.

CAA38037.1 X54103 *Plastid Petunia x hybrida*  
heat shock protein. hsp21.

AAF19022.1 AF197942 *Funaria hygrometrica*  
chloroplast-localized small heat shock protein 22. CPsHSP22.

AAB49626.1 U59917 *Lycopersicon esculentum*  
chromoplast-associated hsp20. pTOM111. small molecular weight heat shock protein.

AAB07023.1 U66300 *Chloroplast Lycopersicon esculentum*  
heat shock protein. HSP21.

BAA29064.1 D88584 *Nicotiana tabacum*  
heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein.

AAF19021.1 AF197941 *Funaria hygrometrica*  
chloroplast-localized small heat shock protein. CPsHSP21. CPsHS 21.

BAA78385.1 AB020973 *Oryza sativa*  
heat shock protein 26. Oshsp26. chloroplast-localized small heat shock protein.

CAA41219.1 X58280 *Triticum aestivum*  
heat shock protein 26.6. Tahsp26.6.

AAC96315.1 AF097657 *Triticum aestivum*  
heat shock protein HSP26. hsp26.6. similar to the *Triticum aestivum* hsp26.6G2 protein encoded by the sequence presented in GenBank Accession Number L41503; 26 kDa protein.

AAC96316.1 AF097658 *Triticum aestivum*  
heat shock protein HSP26. hsp26.6. 26 kDa protein.

AAC96314.1 AF097656 *Triticum aestivum*  
heat shock protein HSP26. hsp26.6. 26 kDa protein.

CAA47745.1 X67328 *Triticum aestivum*  
heat shock protein 26.6B. hsp 26.6B.

AAC96317.1 AF097659 *Triticum aestivum*  
heat shock protein HSP26. hsp26.6. 26 kDa protein.

AAA33477.1	L28712	Zea mays
heat shock protein 26. HSP26. plastid-localized low molecular weight hsp.		
BAA29066.1	AB006043	Nicotiana sylvestris
heat shock protein 26. hsp26. plastid-localized small heat shock protein.		
BAA29067.1	AB006044	Nicotiana tomentosiformis
heat shock protein 26. hsp26. plastid-localized small heat shock protein.		
BAA29065.1	AB006041	Nicotiana tabacum
heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein 26.		
AAC01570.1	AF019144	Agrostis stolonifera var. palustris
low molecular weight heat shock protein.		
AAD30452.1	AF123255	Lycopersicon esculentum
17.7 kD class I small heat shock protein. HSP17.7.		
CAA39603.1	X56138	Lycopersicon esculentum
small heat shock protein (class I).		
AAD30453.1	AF123256	Lycopersicon esculentum
17.8 kD class I small heat shock protein. HSP17.8.		
AAD30454.1	AF123257	Lycopersicon esculentum
17.6 kD class I small heat shock protein. HSP17.6.		
AAD49336.1	AF166277	Nicotiana tabacum
low molecular weight heat-shock protein. LHS-1. TLHS-1.		
AAF34133.1	AF161179	Malus x domestica
low molecular weight heat shock protein. Hsp1.		
AAC39360.1	U63631	Fragaria x ananassa
LMW heat shock protein.		
AAA61632.1	U08601	Papaver somniferum
low molecular weight heat-shock protein.		
CAA08908.1	AJ009880	Castanea sativa
molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.		
AAA33975.1	M11395	Glycine max
small heat shock protein.		
CAA63570.1	X92983	Pseudotsuga menziesii
low molecular weight heat-shock protein.		
AAB03893.1	M11318	Glycine max
17.5 kd heat shock protein Gmhsp17.6L.		
CAA25578.1	X01104	Glycine max
heat shock protein 6871 (aa 1-153).		
AAB72109.1	AF022217	Brassica rapa
low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.		
CAA46641.1	X65725	Zea mays
heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.		
CAB08441.1	Z95153	Helianthus annuus
17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.		

AAA33974.1	M11317	Glycine max 17.6 kd heat shock protein Gmhsp17.6L.
SEQ ID NO: 588		
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
AAA19701.1	L24438	Thlaspi arvense cytochrome P450.
AAC39318.1 AF029858 Sorghum bicolor second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.		
BAB40323.1	AB037244	Asparagus officinalis cytochrome P450. ASPI-1.
BAB40324.1	AB037245	Asparagus officinalis cytochrome P450. ASPI-2.
AAB94589.1	AF022460	Glycine max CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
AAB94584.1	AF022157	Glycine max capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
AAB61965.1	U48435	Solanum chacoense putative cytochrome P450.
AAF27282.1	AF122821	Capsicum annuum cytochrome P450. PepCYP.
CAB56503.1	AJ238612	Catharanthus roseus cytochrome P450.
AAD47832.1	AF166332	Nicotiana tabacum cytochrome P450.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAB61964.1	U48434	Solanum chacoense putative cytochrome P450.
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
CAA50645.1	X71654	Solanum melongena P450 hydroxylase.
BAA03635.1	D14990	Solanum melongena Cytochrome P-450EG4.

CAA50312.1 X70981 *Solanum melongena*  
P450 hydroxylase. CYPEG2.

CAA71514.1 Y10490 *Glycine max*  
putative cytochrome P450.

AAB69644.1 AF000403 *Lotus japonicus*  
putative cytochrome P450. LjNP450.

CAA70576.1 Y09424 *Nepeta racemosa*  
cytochrome P450. CYP71A6.

AAD44151.1 AF124816 *Mentha x piperita*  
cytochrome p450 isoform PM17.

AAK38084.1 AF321860 *Lolium rigidum*  
putative cytochrome P450.

CAA83941.1 Z33875 *Mentha x piperita*  
cytochrome P-450 oxidase.

AAK38083.1 AF321859 *Lolium rigidum*  
putative cytochrome P450.

AAD44152.1 AF124817 *Mentha x piperita*  
cytochrome p450 isoform PM2.

BAB39252.1 AP002968 *Oryza sativa*  
putative cytochrome P450. P0416G11.1.

AAD44150.1 AF124815 *Mentha spicata*  
cytochrome p450.

AAK38087.1 AF321863 *Lolium rigidum*  
putative cytochrome P450.

AAK38082.1 AF321858 *Lolium rigidum*  
putative cytochrome P450.

CAA57423.1 X81829 *Zea mays*  
cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.

CAA72208.1 Y11404 *Zea mays*  
cytochrome p450. cyp71c2.

CAC27827.1 AJ295719 *Catharanthus roseus*  
geraniol hydroxylase. cytochrome P450. cyp71.

AAG44132.1 AF218296 *Pisum sativum*  
cytochrome P450. P450 isolog.

AAK38088.1 AF321864 *Lolium rigidum*  
putative cytochrome P450.

AAG14963.1 AF214009 *Brassica napus*  
cytochrome p450-dependent monooxygenase. BNF5H3.

CAA57424.2 X81830 *Zea mays*  
cytochrome P450. CYP71C3. family CYP71, subfamily CYP71C.

CAA72207.1 Y11403 *Zea mays*  
cytochrome p450. cyp71c3.

AAG14962.1 AF214008 *Brassica napus*  
cytochrome p450-dependent monooxygenase. BNF5H2.

AAG14961.1 AF214007 *Brassica napus*  
cytochrome p450-dependent monooxygenase. BNF5H1.

BAA12159.1 D83968 *Glycine max*  
Cytochrome P-450 (CYP93A1).

BAB40322.1 AB036772 *Triticum aestivum*  
cytochrome P450. N-1.

SEQ ID NO: 593

BAA09645.1 D63331 *Nicotiana tabacum*  
Indole-3-acetonitrile hydrolysis. nitrilase. TNIT4. Indole-3-acetonitrile hydrolysis, indole-3-acetic acid biosynthesis.

BAA11770.1 D83078 *Nicotiana tabacum*  
indole-3-acetonitrile hydrolysis. nitrilase. TNIT4B. indole-3-acetonitrile hydrolysis, indole-3-acetic acid biosynthesis.

BAA77679.1 AB027054 *Oryza sativa*  
nitrilase-like protein. ONIT4.

SEQ ID NO: 595

AAG01147.1 AF283816 *Pinus taeda*  
calreticulin. calcium-binding protein.

CAA05161.1 AJ002057 *Beta vulgaris*  
calreticulin.

AAB71419.1 U74630 *Ricinus communis*  
calreticulin.

AAB71420.1 U74631 *Ricinus communis*  
endoplasmic reticulum calcium binding protein. calreticulin.

CAA95999.1 Z71395 *Nicotiana plumbaginifolia*  
ER Ca<sup>2+</sup> binding protein. calreticulin. cal1.

AAD17490.1 AF052040 *Berberis stolonifera*  
possible molecular chaperon. calreticulin. calcium binding protein of the endoplasmic reticulum.

AAD32207.1 AF134733 *Prunus armeniaca*  
calcium-binding protein calreticulin.

CAA61939.1 X89813 *Zea mays*  
Calreticulin precursor.

AAA32948.1 L27348 *Hordeum vulgare*  
calcium binding protein. calreticulin. CRH1.

AAA32949.1 L27349 *Hordeum vulgare*  
calcium binding protein. calreticulin. CRH2.

AAF01470.1 AF190454 *Zea mays*  
calreticulin. CRT. calcium binding protein.

CAB54526.1 AJ000765 *Chlamydomonas reinhardtii*  
calreticulin.

AAB70919.1 AF019376 *Brassica napus*  
calreticulin. Crt1. calcium binding protein; similar to *A. thaliana* calreticulin encoded by GenBank Accession Number U66343.

BAA85118.1 AB018243 *Solanum melongena*  
calreticulin-like protein. EEF22.

CAA54975.1 X78057 *Zea mays*  
calreticulin. CRH.

CAA57914.1 X82578 *Parthenium argentatum*  
calreticulin. 111R.

AAK15502.1 AF325720 *Pennisetum ciliare*  
calreticulin-like protein. Pcp4.

BAA77025.1 AB026251 *Lithospermum erythrorhizon*  
calreticulin.

SEQ ID NO: 596

BAA12206.1 D84061 *Spinacia oleracea*  
phosphoserine aminotransferase.

SEQ ID NO: 597

AAF73124.1 AF148534 *Lycopersicon esculentum*  
whitefly-induced gp91-phox. Wf1. mammalian gp91-phox homolog; respiratory burst oxidase homolog; putative NADPH oxidase; similar to neutrophil NADPH oxidase gp91-phox subunit; similar to *Arabidopsis thaliana* Rboh and *Oryza sativa* Rboh; similar to *Caenorhabditis elegans* PhoX-like proteins.

AAF73104.1 AF147783 *Lycopersicon esculentum*  
whitefly-induced gp91-phox. Wf1. mammalian gp91-phox homolog; respiratory burst oxidase homolog; putative NADPH oxidase; similar to neutrophil NADPH oxidase gp1-phox subunit; similar to *Arabidopsis thaliana* Rboh and *Oryza sativa* Rboh.

AAD25300.1 AF088276 *Lycopersicon esculentum*  
NADPH oxidase. RBOH1. gp91; phox homolog.

AAB87790.1 AF015302 *Oryza sativa*  
RbohAOsp. putative NADPH oxidase; intrinsic plasma membrane protein; similar to the neutrophil NADPH oxidase gp91phox subunit; contains RanGAP1 domain; similar to *O. sativa* NAD(P)H oxidase sequence with GenBank Accession Number X93301.

CAA63704.1 X93301 *Oryza sativa*  
NAD(P)H oxidase. rbohA.

AAD24966.1 AF109150 *Lycopersicon esculentum*  
NADPH oxidase. gp91; phox homolog.

AAD25225.1 AF088279 *Potamogeton crispus*  
NADPH oxidase. RBOH1. gp91; phox homolog.

SEQ ID NO: 599

CAC21424.1 AJ278332 *Lycopersicon esculentum*  
involved in octadecanoid biosynthesis. 12-oxophytodienoate reductase 3. opr3.

BAB40340.1 AB044940 *Pisum sativum*  
12-oxophytodienoic acid 10, 11-reductase. OPDAR.

CAB43506.1 AJ242551 *Lycopersicon esculentum*  
involved in jasmonic acid biosynthesis. 12-oxophytodienoate reductase. opr.

CAC21423.1 AJ278331 *Lycopersicon esculentum*  
involved in octadecanoid biosynthesis. putative 12-oxophytodienoate reductase 2. opr2.

CAB97122.1 AJ297421 *Daucus carota*  
oxidoreductase. putative 12-oxophytodienoate reductase. opr2.

SEQ ID NO: 602

AAB37246.1 U58971 *Nicotiana tabacum*  
calmodulin-binding protein. TCB60.

SEQ ID NO: 603

AAK15006.1 AF233433 *Brassica napus*  
arginase. similar to *Arabidopsis thaliana* and *Glycine max* arginase.

AAK07744.1 AF130440 *Pinus taeda*  
converts L-arginine to L-ornithine and urea. arginase. ARS20. L-arginine amidinohydrolase.

AAC04613.1 AF035671 *Glycine max*  
hydrolysis of L-Arg to L-Orn and urea. arginase. pAG1. L-Arg amidinohydrolase.

SEQ ID NO: 605

CAA81210.1 Z26251 *Helianthus tuberosus*  
Catalyzes the reduction of cytochrome P450 in microsomes. NADPH-ferrihemoprotein reductase.

AAB02721.1 U58629 *Helianthus tuberosus*  
NADPH-ferrihemoprotein oxidoreductase. HTR2. NADPH-cytochrome P450 reductase isoform.

CAC27143.1 AJ132538 *Picea abies*  
NADPH-cytochrome P450 reductase.

AAA79131.1 U10545 *Chlamydomonas reinhardtii*  
ferredoxin-NADP<sup>+</sup> reductase. fnr.

CAA55406.1 X78851 *Chlamydomonas reinhardtii*  
ferredoxin NADP reductase.

AAB40978.1 U22328 *Volvox carteri*  
ferredoxin-NADP<sup>+</sup> reductase. fnr. FNR.

AAA33029.1 M25528 *Mesembryanthemum crystallinum*  
ferredoxin-NADP<sup>+</sup> reductase precursor (fnrA; EC 1.6.7.1).

CAA30978.1 X12446 *Pisum sativum*  
ferredoxin-NADH<sup>+</sup> reductase preprotein (AA -52 to 308).

BAA13417.1 D87547 *Oryza sativa*  
precursor ferredoxin-NADP<sup>+</sup> oxidoreductase.

AAA21758.1 U14956 *Vicia faba*  
photosynthetic electron transport. ferredoxin NADP<sup>+</sup> reductase precursor. fnr.

AAA34029.1 M86349 *Spinacia oleracea*  
ferredoxin-NADP oxidoreductase. precursor protein.

CAB71293.1 AJ250378 *Capsicum annuum*  
chloroplast ferredoxin-NADP<sup>+</sup> oxidoreductase precursor. fnr.

CAA74359.1	Y14032	Nicotiana tabacum ferredoxin--NADP(+) reductase. fnr.
BAA88236.1	AB035644	Zea mays NADP+ oxidoreductase. ferredoxin. L-FNRI.
BAA88237.1	AB035645	Zea mays NADP+ oxidoreductase. ferredoxin. L-FNRII.
BAA20365.1	AB004307	Nicotiana tabacum ferredoxin-NADP oxidoreductase.
BAA07479.1	D38445	Oryza sativa root ferredoxin-NADP+ reductase. root FNR. nitrate assimilation pathway.
BAA02248.1	D12815	Oryza sativa ferredoxin-NADP+ reductase enzyme.
BAA04232.1	D17410	Oryza sativa ferredoxin-NADP+ reductase.
BAA90642.1	AP001129	Oryza sativa ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; Similar to Oryza sativa, ferredoxin-NADP+ reductase. (D17790).
BAA85425.1	AP000616	Oryza sativa ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790).
BAA04616.1	D17790	Oryza sativa ferredoxin-NADP+ reductase.
AAB40034.1	U10418	Zea mays ferredoxin-NADP reductase precursor.
CAA67796.1	X99419	Pisum sativum ferredoxin NADP oxidoreductase.
AAK09367.1	AF321525	Pisum sativum ferredoxin-NADP+ reductase. FNR.
AAK09370.1	AF321528	Pisum sativum ferredoxin-NADP+ reductase. FNR.
AAK09369.1	AF321527	Pisum sativum ferredoxin-NADP+ reductase. FNR.
AAK09368.1	AF321526	Pisum sativum ferredoxin-NADP+ reductase. FNR.

SEQ ID NO: 606

BAA82107.1	AB022693	Nicotiana tabacum transcription factor. NtWRKY1.
AAC31956.1	AF080595	Pimpinella brachycarpa zinc finger protein. ZFP1. WRKY1.
AAC49527.1	U48831	Petroselinum crispum WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

AAD55974.1 AF121353 *Petroselinum crispum*  
zinc-finger type transcription factor WRKY1. WRKY1.

BAA77383.1 AB020590 *Nicotiana tabacum*  
transcription factor NtWRKY2.

AAD32677.1 AF140554 *Avena sativa*  
DNA-binding protein WRKY1. wrky1. putative transcription factor.

CAA88326.1 Z48429 *Avena fatua*  
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

BAA86031.1 AB026890 *Nicotiana tabacum*  
transcription factor NtWRKY4.

AAD16139.1 AF096299 *Nicotiana tabacum*  
DNA-binding protein 2. WRKY2. transcription factor.

AAC37515.1 L44134 *Cucumis sativus*  
SPF1-like DNA-binding protein.

AAF23898.1 AF193802 *Oryza sativa*  
zinc finger transcription factor WRKY1.

AAK16171.1 AC079887 *Oryza sativa*  
putative DNA-binding protein. OSJNBa0040E01.10.

AAC49529.1 U58540 *Petroselinum crispum*  
WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.

AAD16138.1 AF096298 *Nicotiana tabacum*  
DNA-binding protein 1. WRKY1. transcription factor.

BAB19096.1 AP002839 *Oryza sativa*  
putative DNA-binding protein homolog. P0688A04.2.

BAB19075.1 AP002744 *Oryza sativa*  
putative DNA-binding protein homolog. P0006C01.17.

AAK16170.1 AC079S87 *Oryza sativa*  
putative DNA binding protein. OSJNBa0040E01.4.

CAB97004.1 AJ278507 *Solanum tuberosum*  
putative transcription factor. WRKY DNA binding protein. WRKY1.

BAB18313.1 AP002865 *Oryza sativa*  
putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).

AAD38283.1 AC007789 *Oryza sativa*  
putative WRKY DNA binding protein. OSJNBa0049B20.9.

BAB40073.1 AP003074 *Oryza sativa*  
putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).

AAC49528.1 U56834 *Petroselinum crispum*  
DNA-binding. WRKY3. WRKY-type DNA-binding protein.

BAB16432.1 AB041520 *Nicotiana tabacum*  
WRKY transcription factor Nt-SubD48. Nt-SubD48.

BAA77358.1 AB020023 *Nicotiana tabacum*  
WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.

AAD32676.1	AF140553	Avena sativa DNA-binding protein WRKY3. wrky3. putative transcription factor.
CAA88331.1	Z48431	Avena fatua binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAG35658.1	AF204925	Petroselinum crispum transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
AAG46150.1	AC018727	Oryza sativa putative DNA-binding protein. OSJNBa0056G17.18.
AAD27591.1	AF121354	Petroselinum crispum binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
AAG35659.1	AF204926	Petroselinum crispum transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.
CAB66338.1	AJ279697	Betula pendula wrky-type DNA binding protein. wrky.
AAF61864.1	AF193771	Nicotiana tabacum DNA-binding protein 4. WRKY4. transcription factor.
AAF61863.1	AF193770	Nicotiana tabacum DNA-binding protein 3. WRKY3. transcription factor.
SEQ ID NO: 608		
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB19337.1	AP003044	Oryza sativa putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
BAA92836.1	AB032473	Brassica oleracea S18 S-locus receptor kinase. SRK18.
AAB61708.1	U93048	Daucus carota somatic embryogenesis receptor-like kinase. SERK.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAD21872.1	AF078082	Phaseolus vulgaris receptor-like protein kinase homolog RK20-1.

CAB41878.1	Y18259	Brassica oleracea
SRK5 protein.	SRK5.	receptor-like kinase.
AAA62232.1	U00443	Brassica napus
S-receptor kinase.	protein contains an immunoglobulin-like domain.	
AAA33000.1	M76647	Brassica oleracea
receptor protein kinase.	SKR6.	
AAG59657.1	AC084319	Oryza sativa
putative protein kinase.	OSJNBA0004B24.20.	
CAB41879.1	Y18260	Brassica oleracea
SRK15 protein.	SRK15.	receptor-like kinase.
CAA73134.1	Y12531	Brassica oleracea
serine/threonine kinase.	BRLK.	
BAB16871.1	AP002537	Oryza sativa
putative protein kinase	APK1A	Arabidopsis thaliana. P0001B06.24. contains ESTs
C22608(R3192),	D25110(R3192).	
BAB18292.1	AP002860	Oryza sativa
putative receptor-like protein kinase.	P0409B08.19.	
BAA06285.1	D30049	Brassica rapa
S-receptor kinase	SRK9.	
BAA21132.1	D88193	Brassica rapa
S-receptor kinase.	SRK9 (B.c).	
CAB89179.1	AJ245479	Brassica napus subsp. napus
ser /thr kinase.	S-locus receptor kinase.	srk.
AAA33008.1	M97667	Brassica napus
serine/threonine kinase receptor.		
CAA67145.1	X98520	Brassica oleracea
receptor-like kinase.	SFR2.	
CAA73133.1	Y12530	Brassica oleracea
serine /threonine kinase.	ARLK.	
AAF66615.1	AF142596	Nicotiana tabacum
LRR receptor-like protein kinase.		
AAF76314.1	AF220603	Lycopersicon esculentum
Fen kinase.	Lescfen.	
AAK11568.1	AF318492	Lycopersicon hirsutum
Pto-like protein kinase	B. LhirPtoB.	
CAA74662.1	Y14286	Brassica oleracea
SFR3.	extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.	
AAB47424.1	U59317	Lycopersicon pimpinellifolium
serine/threonine protein kinase Fen.	Fen.	fenthion sensitivity gene from tomato.
AAB47422.1	U59318	Lycopersicon esculentum
serine/threonine protein kinase Fen.	fen.	allele of Fen, fenthion sensitivity gene from tomato.

AAC48932.1 U13923 *Lycopersicon pimpinellifolium*  
Fen. putative serine/threonine protein kinase; similar to product encoded by *Lycopersicon pimpinellifolium* Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.

AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*  
Fen kinase.

BAA07576.1 D38563 *Brassica rapa*  
receptor protein kinase SRK8.

AAG16628.1 AY007545 *Brassica napus*  
protein serine/threonine kinase BNK1.

CAA97692.1 Z73295 *Catharanthus roseus*  
receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

CAA79355.1 Z18921 *Brassica oleracea*  
S-receptor kinase-like protein.

AAB93834.1 U82481 *Zea mays*  
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

BAA92837.1 AB032474 *Brassica oleracea*  
S60 S-locus receptor kinase. SRK60.

AAA33915.1 L27821 *Oryza sativa*  
receptor type serine/threonine kinase. protein kinase.

SEQ ID NO: 610

BAB17348.1 AP002747 *Oryza sativa*  
putative receptor kinase. P0698G03.32.

BAB17345.1 AP002747 *Oryza sativa*  
putative receptor kinase. P0698G03.29.

BAB17126.1 AP002867 *Oryza sativa*  
putative receptor kinase. P0463F06.16.

BAB39451.1 AP003338 *Oryza sativa*  
putative receptor kinase. OJ1212\_B09.24.

BAB17342.1 AP002747 *Oryza sativa*  
putative receptor kinase. P0698G03.26.

AAC27489.1 AF077130 *Oryza sativa*  
receptor-like protein kinase.

AAF78018.1 AF238474 *Oryza sativa*  
receptor-like kinase. RLG16. protein kinase.

AAC02535.1 AF044260 *Oryza sativa*  
receptor serine/threonine kinase. protein kinase.

BAB39435.1 AP003338 *Oryza sativa*  
putative receptor kinase. OJ1212\_B09.2.

AAD46917.1 AF164021 *Oryza sativa*  
receptor kinase.

BAB39438.1 AP003338 Oryza sativa  
putative receptor kinase. OJ1212\_B09.7.

BAB17339.1 AP002747 Oryza sativa  
putative receptor kinase. P0698G03.23.

AAC49629.1 U51330 Triticum aestivum  
rust resistance kinase Lr10. LRK10.

BAB17321.1 AP002747 Oryza sativa  
putative receptor kinase. P0698G03.1.

BAB17129.1 AP002867 Oryza sativa  
putative receptor kinase. P0463F06.20.

AAF68398.1 AF237568 Oryza sativa  
receptor-like protein kinase. RLG2.

BAB17331.1 AP002747 Oryza sativa  
putative receptor kinase. P0698G03.12.

BAB17139.1 AP002867 Oryza sativa  
putative receptor kinase. P0463F06.31.

AAC01746.1 AF044489 Oryza sativa  
receptor-like protein kinase. drpk1.

AAF78016.1 AF238472 Oryza sativa  
receptor-like kinase. RLG15. protein kinase.

BAB39441.1 AP003338 Oryza sativa  
putative receptor kinase. OJ1212\_B09.11.

BAB17116.1 AP002867 Oryza sativa  
putative receptor kinase. P0463F06.3.

AAF78044.1 AF248493 Oryza sativa  
receptor-like kinase. RLG18. protein kinase.

AAD44029.1 AF085164 Hordeum vulgare  
receptor-like kinase LRK10.

BAB17332.1 AP002747 Oryza sativa  
putative receptor kinase. P0698G03.13. contains ESTs D47575(S13157),AU032665(S13157).

BAB17347.1 AP002747 Oryza sativa  
putative receptor kinase. P0698G03.31. contains ESTs D47575(S13157),AU032665(S13157).

BAB17344.1 AP002747 Oryza sativa  
putative receptor kinase. P0698G03.28. contains ESTs D47575(S13157),AU032665(S13157).

BAB17337.1 AP002747 Oryza sativa  
putative receptor kinase. P0698G03.21. contains ESTs D47575(S13157),AU032665(S13157).

BAB17335.1 AP002747 Oryza sativa  
putative receptor kinase. P0698G03.17. contains ESTs D47575(S13157),AU032665(S13157).

BAB17115.1 AP002867 Oryza sativa  
putative receptor kinase. P0463F06.2.

BAB39440.1 AP003338 Oryza sativa  
putative receptor kinase. OJ1212\_B09.10.

BAB39437.1 AP003338 Oryza sativa  
receptor-like kinase. OJ1212\_B09.6.

AAF78019.1 AF238475 Oryza sativa  
receptor-like kinase. RLG17. protein kinase.

BAB17127.1 AP002867 Oryza sativa  
putative receptor kinase. P0463F06.17.

AAD46916.1 AF164020 Oryza sativa  
receptor kinase.

AAF78021.1 AF238477 Oryza sativa  
receptor-like kinase. RLG5. protein kinase.

AAD46417.1 AF100767 Oryza sativa  
receptor-like kinase. 8ARK3. similar to wheat ARK1AS.

AAD46415.1 AF100765 Oryza sativa  
receptor-like kinase. 8ARK1. similar to wheat ARK1AS.

BAB17128.1 AP002867 Oryza sativa  
putative receptor kinase. P0463F06.18.

AAF68400.1 AF237570 Oryza sativa  
receptor-like protein kinase. RLG3.

BAB17323.1 AP002747 Oryza sativa  
putative receptor kinase. P0698G03.3.

BAB17131.1 AP002867 Oryza sativa  
putative receptor kinase. P0463F06.22.

AAF68397.1 AF237567 Oryza sativa  
receptor-like protein kinase. RLG1.

AAF78015.1 AF238471 Oryza sativa  
receptor-like kinase. RLG10. protein kinase.

AAD43962.1 U78762 Triticum aestivum  
receptor-like kinase ARK1AS. ARK1AS.

SEQ ID NO: 611

BAA78764.1 AB023482 Oryza sativa  
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar  
to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAK11674.1 AF339747 Lophopyrum elongatum  
protein kinase. ESI47.

AAF43496.1 AF131222 Lophopyrum elongatum  
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and  
ABA treatment.

AAG16628.1 AY007545 Brassica napus  
protein serine/threonine kinase BNK1.

BAA94509.1 AB041503 Populus nigra  
protein kinase 1. PnPK1.

BAA94510.1 AB041504 Populus nigra  
protein kinase 2. PnPK2.

BAB07999.1 AP002525 *Oryza sativa*  
putative protein kinase. P0462H08.22. contains EST C22619(S11214).

BAB03429.1 AP002817 *Oryza sativa*  
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

BAA87853.1 AP000816 *Oryza sativa*  
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

BAB16871.1 AP002537 *Oryza sativa*  
putative protein kinase APK1A *Arabidopsis thaliana*. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

BAB39409.1 AP002901 *Oryza sativa*  
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

CAB51834.1 00069 *Oryza sativa*  
I1332.5. contains eukaryotic protein kinase domain PF.

BAB21240.1 AP002953 *Oryza sativa*  
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

AAK00425.1 AC069324 *Oryza sativa*  
Putative protein kinase. OSJN<sub>B</sub>a0071K19.11.

BAB39873.1 AP002882 *Oryza sativa*  
putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

AAK11567.1 AF318491 *Lycopersicon hirsutum*  
Pto-like protein kinase F. LhirPtoF.

BAA90808.1 AP001168 *Oryza sativa*  
Similar to putative receptor-like protein kinase (AL035679).

AAK21965.1 AY028699 *Brassica napus*  
receptor protein kinase PERK1.

AAC48932.1 U13923 *Lycopersicon pimpinellifolium*  
Fen. putative serine/threonine protein kinase; similar to product encoded by *Lycopersicon pimpinellifolium* Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.

AAB47424.1 U59317 *Lycopersicon pimpinellifolium*  
serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.

AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*  
Fen kinase.

AAK11566.1 AF318490 *Lycopersicon hirsutum*  
Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.

AAG03090.1 AC073405 *Oryza sativa*  
Similar to an *Arabidopsis* somatic embryogenesis receptor-like kinase (AC007504).

AAF76314.1 AF220603 *Lycopersicon esculentum*  
Fen kinase. Lescfen.

AAB47421.1 U59316 *Lycopersicon esculentum*  
serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

AAF76313.1 AF220603 *Lycopersicon esculentum*  
Pto kinase. LescPth5.

AAB47422.1 U59318 *Lycopersicon esculentum*  
serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.

AAG59657.1 AC084319 *Oryza sativa*  
putative protein kinase. OSJNBa0004B24.20.

AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*  
Pto kinase.

AAB47423.1 U59315 *Lycopersicon pimpinellifolium*  
serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.

AAC48914.1 U02271 *Lycopersicon pimpinellifolium*  
protein kinase.

AAK11568.1 AF318492 *Lycopersicon hirsutum*  
Pto-like protein kinase B. LhirPtoB.

BAB21241.1 AP002953 *Oryza sativa*  
Putative Pto kinase interactor 1. P0426D06.21. contains ESTs  
AU108280(E0721),D48017(S13927).

AAC27894.1 AF023164 *Zea mays*  
leucine-rich repeat transmembrane protein kinase 1. ltk1.

AAF91337.1 AF249318 *Glycine max*  
Pt1 kinase-like protein. Pt1b. protein kinase.

AAC61805.1 U28007 *Lycopersicon esculentum*  
serine/threonine protein kinase. Pto kinase interactor 1. Pt1. Pt1 kinase.

CAA97692.1 Z73295 *Catharanthus roseus*  
receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser.  
Mechanism: autophosphorylation in cis.

AAF91336.1 AF249317 *Glycine max*  
Pt1 kinase-like protein. Pt1a. protein kinase.

AAF66615.1 AF142596 *Nicotiana tabacum*  
LRR receptor-like protein kinase.

AAB61708.1 U93048 *Daucus carota*  
somatic embryogenesis receptor-like kinase. SERK.

AAK11569.1 AF318493 *Lycopersicon hirsutum*  
Pto-like protein kinase D. LhirPtoD.

BAA92221.1 AP001278 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).

BAA87852.1 AP000816 *Oryza sativa*  
Similar to putative Ser/Thr protein kinase. (AC004218).

AAC27895.1	AF023165	Zea mays leucine-rich repeat transmembrane protein kinase 2. ltk2.	SEQ ID NO: 612
CAA54613.1	X77463	Manihot esculenta UTP-glucose glucosyltransferase. CGT6.	
CAA54609.1	X77459	Manihot esculenta UTP-glucose glucosyltransferase. CGT1.	
CAA54611.1	X77461	Manihot esculenta UTP-glucose glucosyltransferase. CGT2.	
CAA54612.1	X77462	Manihot esculenta UTP-glucose glucosyltransferase. CGT5.	
BAB17182.1	AP002843	Oryza sativa putative UTP-glucose glucosyltransferase. P0407B12.19.	
BAB17176.1	AP002843	Oryza sativa putative UTP-glucose glucosyltransferase. P0407B12.13.	
CAB56231.1	Y18871	Dorotheanthus bellidiformis betanidin-5-O-glucosyltransferase.	
BAA83484.1	AB031274	Scutellaria baicalensis UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.	
AAB36653.1	U32644	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS5a.	
AAK28303.1	AF346431	Nicotiana tabacum phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.	
CAA59450.1	X85138	Lycopersicon esculentum twi1. homologous to glucosyltransferases.	
AAB36652.1	U32643	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS10a.	
AAK28304.1	AF346432	Nicotiana tabacum phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.	
BAA89009.1	AB027455	Petunia x hybrida anthocyanin 5-O-glucosyltransferase. PH1.	
AAG25643.1	AF303396	Phaseolus vulgaris UDP-glucosyltransferase HRA25. putative; defense associated.	
AAF61647.1	AF190634	Nicotiana tabacum UDP-glucose: salicylic acid glucosyltransferase. SA-GTase.	
BAA93039.1	AB033758	Citrus unshiu limonoid UDP-glucosyltransferase. LGTase.	
AAB48444.1	U82367	Solanum tuberosum UDP-glucose glucosyltransferase.	
AAD21086.1	AF127218	Forsythia x intermedia adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.	

AAK16175.1 AC079887 *Oryza sativa*  
 putative glucosyltransferase. OSJN<sub>B</sub>a0040E01.15.

CAC09351.1 AL442007 *Oryza sativa*  
 putative glucosyltransferase. H0212B02.7.

AAD04166.1 AF101972 *Phaseolus lunatus*  
 catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

AAF17077.1 AF199453 *Sorghum bicolor*  
 UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.

BAA12737.1 D85186 *Gentiana triflora*  
 UDP-glucose:flavonoid-3-glucosyltransferase.

BAB07962.1 AP002524 *Oryza sativa*  
 putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).

BAA36421.1 AB013596 *Perilla frutescens*  
 UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.

CAA54610.1 X77460 *Manihot esculenta*  
 UTP-glucose glucosyltransferase. CGT4.

AAF98390.1 AF287143 *Brassica napus*  
 catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

BAA36423.1 AB013598 *Verbena x hybrida*  
 UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

CAA30760.1 X07937 *Zea mays*  
 UDPglucose flavonoid glycosyl transferase. Bz-W22.

CAA30761.1 X07940 *Zea mays*  
 UDPglucose flavonoid glycosyl-transferase. Bz-McC.

CAA31855.1 X13500 *Zea mays*  
 UDPglucose:flavonol 3-O-glucosyltransferase.

BAA19659.1 AB002818 *Perilla frutescens*  
 flavonoid 3-O-glucosyltransferase. UDP glucose.

BAA89008.1 AB027454 *Petunia x hybrida*  
 anthocyanidin 3-O-glucosyltransferase. PGT8.

AAK16172.1 AC079887 *Oryza sativa*  
 putative glucosyltransferase. OSJN<sub>B</sub>a0040E01.14.

SEQ ID NO: 613

CAA54609.1 X77459 *Manihot esculenta*  
 UTP-glucose glucosyltransferase. CGT1.

CAA54613.1 X77463 *Manihot esculenta*  
 UTP-glucose glucosyltransferase. CGT6.

CAA54611.1	X77461	<i>Manihot esculenta</i> UTP-glucose glucosyltransferase. CGT2.
CAA54612.1	X77462	<i>Manihot esculenta</i> UTP-glucose glucosyltransferase. CGT5.
BAB17182.1	AP002843	<i>Oryza sativa</i> putative UTP-glucose glucosyltransferase. P0407B12.19.
BAB17176.1	AP002843	<i>Oryza sativa</i> putative UTP-glucose glucosyltransferase. P0407B12.13.
CAB56231.1	Y18871	<i>Dorotheanthus bellidiformis</i> betanidin-5-O-glucosyltransferase.
AAB36653.1	U32644	<i>Nicotiana tabacum</i> immediate-early salicylate-induced glucosyltransferase. IS5a.
AAK28303.1	AF346431	<i>Nicotiana tabacum</i> phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAB36652.1	U32643	<i>Nicotiana tabacum</i> immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	<i>Nicotiana tabacum</i> phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
CAA59450.1	X85138	<i>Lycopersicon esculentum</i> twi1. homologous to glucosyltransferases.
BAA83484.1	AB031274	<i>Scutellaria baicalensis</i> UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAF61647.1	AF190634	<i>Nicotiana tabacum</i> UDP-glucose: salicylic acid glucosyltransferase. SA-GTase.
BAA93039.1	AB033758	<i>Citrus unshiu</i> limonoid UDP-glucosyltransferase. LGTase.
AAB48444.1	U82367	<i>Solanum tuberosum</i> UDP-glucose glucosyltransferase.
BAA89009.1	AB027455	<i>Petunia x hybrida</i> anthocyanin 5-O-glucosyltransferase. PH1.
BAA36421.1	AB013596	<i>Perilla frutescens</i> UDP-glucose:anthocysnin 5-O-glucosyltransferase. PF3R4.
CAC09351.1	AL442007	<i>Oryza sativa</i> putative glucosyltransferase. H0212B02.7.
BAA12737.1	D85186	<i>Gentiana triflora</i> UDP-glucose:flavonoid-3-glucosyltransferase.
AAG25643.1	AF303396	<i>Phaseolus vulgaris</i> UDP-glucosyltransferase HRA25. putative; defense associated.
AAD04166.1	AF101972	<i>Phaseolus lunatus</i> catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

CAA54610.1 X77460 *Manihot esculenta*

UTP-glucose glucosyltransferase. CGT4.

AAF98390.1 AF287143 *Brassica napus*

catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

AAK16172.1 AC079887 *Oryza sativa*

putative glucosyltransferase. OSJNBa0040E01.14.

BAA36423.1 AB013598 *Verbena x hybrida*

UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

AAD21086.1 AF127218 *Forsythia x intermedia*

adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.

AAF17077.1 AF199453 *Sorghum bicolor*

UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.

AAK16175.1 AC079887 *Oryza sativa*

putative glucosyltransferase. OSJNBa0040E01.15.

BAB07962.1 AP002524 *Oryza sativa*

putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).

CAA31855.1 X13500 *Zea mays*

UDPGlucose:flavonol 3-O-glucosyltransferase.

BAA36422.1 AB013597 *Perilla frutescens*

UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.

BAA89008.1 AB027454 *Petunia x hybrida*

anthocyanidin 3-O-glucosyltransferase. PGT8.

SEQ ID NO: 614

AAD21872.1 AF078082 *Phaseolus vulgaris*

receptor-like protein kinase homolog RK20-1.

CAA73134.1 Y12531 *Brassica oleracea*

serine/threonine kinase. BRLK.

AAB93834.1 U82481 *Zea mays*

KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

AAA33008.1 M97667 *Brassica napus*

serine/threonine kinase receptor.

CAB89179.1 AJ245479 *Brassica napus* subsp. napus

ser /thr kinase. S-locus receptor kinase. srk.

AAA33000.1 M76647 *Brassica oleracea*

receptor protein kinase. SKR6.

BAA23676.1 AB000970 *Brassica rapa*

receptor kinase 1. BcRK1.

BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c.).
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
BAA92837.1	AB032474	Brassica oleracea S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa receptor protein kinase SRK12.
BAA07576.1	D38563	Brassica rapa receptor protein kinase SRK8.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
CAA74662.1	Y14286	Brassica oleracea SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAB21001.1	AB054061	Brassica rapa S locus receptor kinase. SRK22.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
CAB41879.1	Y18260	Brassica oleracea SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea SRK5 protein. SRK5. receptor-like kinase.
BAA92836.1	AB032473	Brassica oleracea S18 S-locus receptor kinase. SRK18.
BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
AAD52097.1	AF088885	Nicotiana tabacum receptor-like kinase CHRK1. Chrk1.
AAA33915.1	L27821	Oryza sativa receptor type serine/threonine kinase. protein kinase.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBA0071K19.11.
BAA94529.2	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA94509.1	AB041503	Populus nigra protein kinase 1. PnPK1.
BAA94510.1	AB041504	Populus nigra protein kinase 2. PnPK2.
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAG03090.1	AC073405	Oryza sativa Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA94518.1	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAB07904.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.12.
SEQ ID NO: 619		
CAA72092.1	Y11209	Nicotiana tabacum protein disulfide-isomerase precursor. PDI.
AAG13988.1	AF298829	Prunus avium putative protein disulfide-isomerase. PDI.
AAD02069.1	AF036939	Chlamydomonas reinhardtii redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.
AAC49896.1	AF027727	Chlamydomonas reinhardtii involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.
AAD55566.1	AF110784	Volvox carteri f. nagariensis protein disulfide isomerase precursor. pdi.
AAB08519.1	L39014	Zea mays protein disulfide isomerase. pdi. putative.

AAA70344.1 L33250 *Hordeum vulgare*  
 catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

AAA70345.1 L33251 *Hordeum vulgare*  
 catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

CAC21230.1 AJ277379 *Triticum turgidum* subsp. *durum*  
 catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

AAA19660.1 U11496 *Triticum aestivum*  
 protein disulfide isomerase. PDI.

CAC21231.1 AJ277380 *Triticum turgidum* subsp. *durum*  
 catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

CAC21229.1 AJ277378 *Triticum turgidum* subsp. *durum*  
 catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

CAC21228.1 AJ277377 *Triticum turgidum* subsp. *durum*  
 catalyzes the formation of disulfide bonds. protein disulfide isomerase. Pdi.

AAB05641.1 U41385 *Ricinus communis*  
 protein disulphide isomerase PDI. molecular chaperone.

CAA77575.1 Z11499 *Medicago sativa*  
 protein disulfide isomerase.

AAD28260.1 AF131223 *Datisca glomerata*  
 protein disulfide isomerase homolog. PDI.

AAA70346.1 L33252 *Hordeum vulgare*  
 catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

BAA92322.1 AB039278 *Oryza sativa*  
 protein disulfide isomerase. Pdi.

BAA77026.1 AB026252 *Lithospermum erythrorhizon*  
 disulfide-isomerase precursor.

AAC79709.1 AF093614 *Acetabularia acetabulum*  
 putative protein disulfide isomerase.

SEQ ID NO: 620

CAA64413.1 X94943 *Lycopersicon esculentum*  
 peroxidase. cevi16.

AAA32676.1 M37637 *Arachis hypogaea*  
 cationic peroxidase. PNC2.

BAA82307.1 AB027753 *Nicotiana tabacum*  
 peroxidase.

AAB67737.1 L77080 *Stylosanthes humilis*  
 cationic peroxidase.

AAD37429.2 AF149279 *Phaseolus vulgaris*  
 peroxidase 4 precursor. FBP4. secretory peroxidase.

CAA71494.1 Y10468 *Spinacia oleracea*  
 peroxidase. prxr7.

AAD37375.1	AF145349	Glycine max peroxidase. Prx3.
AAF63024.1	AF244921	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAB39274.1	AP002971	Oryza sativa putative peroxidase. P0537A05.2.
AAA65637.1	L13654	Lycopersicon esculentum peroxidase. TPX1.
CAA40796.1	X57564	Armoracia rusticana peroxidase. peroxidase precursor.
AAD11482.1	U51192	Glycine max peroxidase precursor. sEPa2.
CAA80502.1	Z22920	Spirodela polyrrhiza peroxidase.
BAA77387.1	AB024437	Scutellaria baicalensis peroxidase 1.
CAA59485.1	X85228	Triticum aestivum peroxidase. POX2.
BAA07663.1	D42064	Nicotiana tabacum cationic peroxidase isozyme 38K precursor.
BAA11853.1	D83225	Populus nigra peroxidase.
BAA07664.1	D42065	Nicotiana tabacum cationic peroxidase isozyme 40K precursor.
AAD37430.1	AF149280	Phaseolus vulgaris peroxidase 5 precursor. FBP5. secretory peroxidase.
AAD11481.1	U51191	Glycine max peroxidase precursor. sEPa1.
CAB94692.1	AJ242742	Ipomoea batatas Removal of H <sub>2</sub> O <sub>2</sub> , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
BAA03644.1	D14997	Oryza sativa peroxidase.
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
BAA92500.1	AP001383	Oryza sativa ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).

BAA90365.1 AP001081 Oryza sativa  
ESTs D24550(R2151),D24265(R1609),AU031848(R2151) correspond to a region of the predicted gene. Similar to cationic peroxidase isozyme 40K precursor (D42065).

BAA89584.1 AP001073 Oryza sativa  
ESTs D24550(R2151),D24265(R1609),AU031848(R2151) correspond to a region of the predicted gene. Similar to cationic peroxidase isozyme 40K precursor (D42065).

AAF34416.1 AF172282 Oryza sativa  
putative peroxidase. DUPR11.5.

AAC49820.1 AF014469 Oryza sativa  
peroxidase. POX5.1. wound inducible.

CAA66034.1 X97348 Populus balsamifera subsp. trichocarpa  
signal for ER. peroxidase.

BAB39281.1 AP002971 Oryza sativa  
putative peroxidase. P0537A05.10. contains ESTs D24657(R2329),AU082066(R2329).

BAA14144.1 D90116 Armoracia rusticana  
peroxidase isozyme.

AAB97734.1 AF014502 Glycine max  
seed coat peroxidase precursor. Ep. H2O2 oxidoreductase; class III plant peroxidase.

CAA37713.1 X53675 Triticum aestivum  
peroxidase.

AAC05277.1 AF049881 Linum usitatissimum  
peroxidase FLXPER4. PER4.

CAA66035.1 X97349 Populus balsamifera subsp. trichocarpa  
signal for ER. peroxidase.

BAA06335.1 D30653 Populus kitakamiensis  
peroxidase.

CAA39486.1 X56011 Triticum aestivum  
peroxidase.

BAA03911.1 D16442 Oryza sativa  
peroxidase.

BAA94962.1 AB042103 Asparagus officinalis  
peroxidase. AspPOX1.

AAC49821.1 AF014470 Oryza sativa  
peroxidase. POXgX9. expressed in roots.

AAD37427.1 AF149277 Phaseolus vulgaris  
peroxidase 1 precursor. FBP1. secretory peroxidase.

CAA76374.2 Y16776 Spinacia oleracea  
peroxidase. prx10.

BAA08499.1 D49551 Oryza sativa  
peroxidase. poxN.

CAA66036.1 X97350 Populus balsamifera subsp. trichocarpa  
signal for ER. peroxidase.

AAA34108.1 J02979 *Nicotiana tabacum*  
lignin-forming peroxidase precursor (EC 1.11.1.7).

CAA62226.1 X90693 *Medicago sativa*  
peroxidase1B. prx1B.

CAA59487.1 X85230 *Triticum aestivum*  
peroxidase. pox4.

SEQ ID NO: 626

CAA98160.1 Z73932 *Lotus japonicus*  
GTP-binding protein. RAB1C. rab1C.

BAA76422.1 AB024994 *Cicer arietinum*  
rab-type small GTP-binding protein.

BAA02116.1 D12548 *Pisum sativum*  
GTP-binding protein.

CAA69701.1 Y08425 *Nicotiana plumbaginifolia*  
small GTP-binding protein. Rab1 subfamily.

AAA80678.1 U38464 *Lycopersicon esculentum*  
small GTP-binding protein. LeRab1A. ; YPT1/Rab1A homolog LeRab1A.

BAA02118.1 D12550 *Pisum sativum*  
GTP-binding protein.

AAB97115.1 U58854 *Glycine max*  
small GTP-binding protein. sra2.

CAA51011.1 X72212 *Nicotiana tabacum*  
ras-related GTP-binding protein. ypt2 homologue.

AAF65510.1 AF108883 *Capsicum annuum*  
small GTP-binding protein.

AAA80680.1 U38466 *Lycopersicon esculentum*  
small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog LeRab1C.

CAA98161.1 Z73933 *Lotus japonicus*  
GTP-binding protein. RAB1D. rab1D.

BAA02117.1 D12549 *Pisum sativum*  
GTP-binding protein.

CAA98162.1 Z73934 *Lotus japonicus*  
GTP-binding protein. RAB1E. rab1E.

AAA50159.1 L27417 *Glycine max*  
GTP binding protein.

AAB28535.1 S66160 *Oryza sativa*  
ric1. ras-related GTP binding protein possessing GTPase activity; This sequence comes from Fig. 1.

CAA98159.1 Z73931 *Lotus japonicus*  
GTP-binding protein. RAB1B. rab1B.

BAA02115.1 D12547 *Pisum sativum*  
GTP-binding protein.

CAA66447.1	X97853	Lotus japonicus GTP-binding protein. RAB1A. rab1A.
AAD10389.1	U35026	Petunia x hybrida Rab1-like small GTP-binding protein.
AAA80679.1	U38465	Lycopersicon esculentum small GTP-binding protein. LeRab1B. ; Ypt1/Rab1A homolog LeRab1B.
BAB07961.1	AP002524	Oryza sativa putative GTP-binding protein. P0406H10.17. contains ESTs D23874(R0480),AU031678(R0480).
CAA98176.1	Z73948	Lotus japonicus GTP-binding protein. RAB8E. rab8E.
CAA89021.1	Z49152	Beta vulgaris GTP-binding. small G protein.
CAA98172.1	Z73944	Lotus japonicus GTP-binding protein. RAB8A. rab8A.
CAA04701.1	AJ001367	Daucus carota small GTP-binding protein. Dc-Rab8.
CAA90080.1	Z49900	Pisum sativum small GTP-binding protein.
AAD46405.1	AF096249	Lycopersicon esculentum ethylene-responsive small GTP-binding protein. ER43.
CAA98174.1	Z73946	Lotus japonicus GTP-binding protein. RAB8C. rab8C.
CAA90082.1	Z49902	Pisum sativum small GTP-binding protein.
CAA49600.1	X69980	Lycopersicon esculentum GTP-binding protein. ypt2.
CAA98175.1	Z73947	Lotus japonicus GTP-binding protein. RAB8D. rab8D.
CAA90081.1	Z49901	Pisum sativum small GTP-binding protein.
AAB17726.1	U38471	Brassica rapa small GTP-binding protein rab. BRAB-1. small GTP-binding protein rab family.
AAA34251.1	L08128	Volvox carteri GTP-binding protein. yptV2.
CAA98173.1	Z73945	Lotus japonicus GTP-binding protein. RAB8B. rab8B.
CAA89049.1	Z49190	Beta vulgaris GTP-binding. small G protein.
CAA98179.1	Z73951	Lotus japonicus GTP-binding protein. RAB11C. rab11C.
AAA34253.1	L08130	Volvox carteri GTP-binding protein. yptV4.

CAA98165.1	Z73937	Lotus japonicus GTP-binding protein. RAB2A. rab2A.
AAA63902.1	U22433	Zea mays GTP binding protein. rab2.
AAA90955.1	U32185	Glycine max vesicular transport. guanine nucleotide regulatory protein. rab2. GTP-binding protein; soyrab.
SEQ ID NO: 628		
AAA87456.1	U22147	Hevea brasiliensis beta-1,3-glucanase. HGN1. hydrolytic enzyme.
CAB38443.1	AJ133470	Hevea brasiliensis beta-1,3-glucanase. hgn1.
AAG24921.1	AF311749	Hevea brasiliensis beta-1,3-glucanase.
AAF44667.1	AF239617	Vitis vinifera hydrolysis of 1,3-beta-D-glucosidic linkages in 1,3-beta-D-glucans. beta-1,3-glucanase. fungal pathogen defense-related protein.
AAA33648.1	L02212	Pisum sativum beta-1,3-glucan hydrolysis. beta-1,3-glucanase. putative.
AAB41551.1	U27179	Medicago sativa subsp. sativa acidic glucanase.
AAB24398.1	S51479	Pisum sativum beta-1,3-glucanase. beta-1,3-glucanase. This sequence comes from Fig. 1B.
CAA37289.1	X53129	Phaseolus vulgaris 1,3,-beta-D-glucanase.
AAA34078.1	M63634	Nicotiana plumbaginifolia regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
AAA51643.1	M23120	Nicotiana plumbaginifolia beta-glucanase precursor.
CAA30261.1	X07280	Nicotiana plumbaginifolia beta-glucanase.
AAA03618.1	M80608	Lycopersicon esculentum beta-1,3-glucanase.
AAC19114.1	AF067863	Solanum tuberosum 1,3-beta-glucan glucanohydrolase. glucanase.
AAA18928.1	U01901	Solanum tuberosum catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA63539.1	M60402	Nicotiana tabacum glucan beta-1,3-glucanase. glucanase GLA.
AAA63540.1	M60403	Nicotiana tabacum glucan-1,3-beta-glucosidase. glucanase GLB.

AAA88794.1 U01900 *Solanum tuberosum*  
catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB1. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.

AAA63541.1 M59442 *Nicotiana tabacum*  
basic beta-1,3-glucanase. glucanase.

AAB82772.2 AF001523 *Musa acuminata*  
beta-1, 3-glucanase. similar to beta-1, 3-glucanase.

AAF08679.1 AF004838 *Musa acuminata*  
beta-1,3-glucanase.

AAA19111.1 U01902 *Solanum tuberosum*  
catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB3. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.

AAC04710.1 AF034106 *Glycine max*  
beta-1,3-glucanase 1. SGlu1.

AAC04714.1 AF034113 *Glycine max*  
beta-1,3-glucanase 8. SGlu8.

CAB91554.1 AJ277900 *Vitis vinifera*  
beta 1-3 glucanase. g1.

AAA34082.1 M20620 *Nicotiana tabacum*  
prepro-beta-1,3-glucanase precursor.

CAA03908.1 AJ000081 *Citrus sinensis*  
glucan hydrolase. beta-1,3-glucanase. gns1.

AAB03501.1 U41323 *Glycine max*  
beta-1,3-glucanase. SGN1.

AAA92013.1 U49454 *Prunus persica*  
beta-1,3-glucanase. Gns1.

AAA33946.1 M37753 *Glycine max*  
beta-1,3-endoglucanase (EC 3.2.1.39).

AAA63542.1 M59443 *Nicotiana tabacum*  
acidic beta-1,3-glucanase. glucanase.

AAF34761.1 AF227953 *Capsicum annuum*  
basic beta-1,3-glucanase. BGLU.

AAD33881.1 AF141654 *Nicotiana tabacum*  
beta-1,3-glucanase. GGL4.

AAG34080.1 AF294849 *Capsicum annuum*  
beta-1,3-glucanase-like protein.

AAF33405.1 AF230109 *Populus x canescens*  
beta-1,3 glucanase. BGLUC.

AAD33880.1 AF141653 Nicotiana tabacum  
beta-1,3-glucanase. GGL1.

CAA57255.1 X81560 Nicotiana tabacum  
(1-)-beta-glucanase. Sp41a.

AAA34053.1 M60464 Nicotiana tabacum  
beta-1,3-glucanase.

SEQ ID NO: 630

AAD37698.1 AF145729 Oryza sativa  
homeodomain leucine zipper protein. Oshox5. transcription factor.

BAA05624.1 D26575 Daucus carota  
transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.

AAF01765.1 AF184278 Glycine max  
homeodomain-leucine zipper protein 57. Hdl57. transcription factor.

CAA64417.1 X94947 Lycopersicon esculentum  
homeobox. VAHOX1.

BAA93465.1 AB028077 Physcomitrella patens  
homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.

BAB18171.1 AB042769 Zinnia elegans  
homeobox-leucine zipper protein. ZeHB3. full length.

BAA93460.1 AB028072 Physcomitrella patens  
homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.

BAA93466.1 AB028078 Physcomitrella patens  
homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.

BAA93461.1 AB028073 Physcomitrella patens  
homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.

BAA05625.1 D26576 Daucus carota  
transcriptiional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.

BAA05622.1 D26573 Daucus carota  
transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.

BAA93467.1 AB028079 Physcomitrella patens  
homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.

BAA93464.1 AB028076 Physcomitrella patens  
homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.

AAD37697.1 AF145728 Oryza sativa  
homeodomain leucine zipper protein. Oshox4. transcription factor.

AAF01764.2 AF184277 Glycine max  
homeodomain-leucine zipper protein 56. Hdl56. transcription factor.

BAA21017.1 D26578 Daucus carota  
transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.

BAB18168.1	AB042766	Zinnia elegans homeobox-leucine zipper protein. ZeHB7. 3'RACE product.
BAA93468.1	AB028080	Physcomitrella patens homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA05623.1	D26574	Daucus carota transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
AAD37699.1	AF145730	Oryza sativa homeodomain leucine zipper protein. Oshox6. transcription factor.
AAD38144.1	AF139497	Prunus armeniaca DNA-binding protein. homeobox leucine zipper protein. HBLZP.
AAA63768.2	AF339748	Helianthus annuus homeobox-leucine zipper protein HAHB-4. Hahb-4.
BAA93463.1	AB028075	Physcomitrella patens homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA64491.1	X95193	Pimpinella brachycarpa transcription activator. homeobox-leucine zipper protein.
CAA64221.1	X94449	Pimpinella brachycarpa transcription activator. homeobox-leucine zipper protein. PHZ4.
CAA64152.1	X94375	Pimpinella brachycarpa transcription activator. homeobox-leucine zipper protein.
AAD37700.1	AF145731	Oryza sativa homeodomain leucine zipper protein. Oshox7. transcription factor.
AAD37695.1	AF145726	Oryza sativa homeodomain leucine zipper protein. Oshox2. transcription factor.
CAA06728.1	AJ005833	Craterostigma plantagineum transcription factor. homeodomain leucine zipper protein. hb-2.
CAA62608.1	X91212	Lycopersicon esculentum HD-ZIP protein. THOM1.
CAA63222.1	X92489	Glycine max transcription activator. homeobox-leucine zipper protein.
CAA65456.2	X96681	Oryza sativa transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	Oryza sativa homeodomain-leucine zipper transcription factor. Hox1. hox1.
SEQ ID NO: 631		
CAC19183.1	AJ291816	Cicer arietinum expansin.
AAD13633.1	AF059489	Lycopersicon esculentum expansin precursor. Exp5.
AAG13983.1	AF297522	Prunus avium expansin 2. Exp2. PruavExp2.

AAF35902.1 AF230333 *Zinnia elegans*  
expansin 3.

AAF32409.1 AF230276 *Triphysaria versicolor*  
alpha-expansin 3.

AAC96080.1 AF049353 *Nicotiana tabacum*  
involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.

AAG13982.1 AF297521 *Prunus avium*  
expansin 1. Exp1. PruavExp1.

AAC33529.1 U93167 *Prunus armeniaca*  
expansin. PA-Exp1.

AAF32411.1 AF230278 *Triphysaria versicolor*  
alpha-expansin 1.

AAF35901.1 AF230332 *Zinnia elegans*  
expansin 2.

AAF21101.1 AF159563 *Fragaria x ananassa*  
expansin. Exp2. ripening regulated.

BAB19676.1 AB029083 *Prunus persica*  
expansin. PchExp1.

AAD47901.1 AF085330 *Pinus taeda*  
expansin.

AAC33530.1 AF038815 *Prunus armeniaca*  
expansin. Exp2.

CAC19184.1 AJ291817 *Cicer arietinum*  
expansin.

AAB40635.1 U64891 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAG32921.1 AF184233 *Lycopersicon esculentum*  
expansin. Exp10.

AAD49956.1 AF167360 *Rumex palustris*  
expansin. EXP1.

AAB40637.1 U64893 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAB40634.1 U64890 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAB37746.1 U30382 *Cucumis sativus*  
expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.

AAB40636.1 U64892 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAC39512.1 AF043284 *Gossypium hirsutum*  
expansin. GhEX1. contains N-terminal signal peptide.

CAB43197.1 AJ239068 *Lycopersicon esculentum*  
cell wall loosening enzyme. expansin2. exp2.

AAC64201.1 AF096776 *Lycopersicon esculentum*  
expansin. LeEXP2.

AAC96081.1 AF049354 *Nicotiana tabacum*  
involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.

CAB46492.1 AJ243340 *Lycopersicon esculentum*  
expansin9. exp9.

AAF17570.1 AF202119 *Marsilea quadrifolia*  
alpha-expansin. EXP1. Mq-EXP1.

AAB81662.1 U85246 *Oryza sativa*  
expansin. Os-EXP4.

AAF62180.1 AF247162 *Oryza sativa*  
alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.

AAB38074.1 U30477 *Oryza sativa*  
induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.

AAD13632.1 AF059488 *Lycopersicon esculentum*  
expansin precursor. Exp4.

AAF32410.1 AF230277 *Triphysaria versicolor*  
alpha-expansin 2.

AAG01875.1 AF291659 *Striga asiatica*  
alpha-expansin 3. Exp3.

CAA04385.1 AJ000885 *Brassica napus*  
Cell wall extension in plants. Expansin.

CAA06271.2 AJ004997 *Lycopersicon esculentum*  
expansin18. exp18.

BAB32732.1 AB049406 *Eustoma grandiflorum*  
expansin. Eg Expansin.

AAC63088.1 U82123 *Lycopersicon esculentum*  
expansin. LeEXP1. fruit ripening regulated expansin.

AAF62182.1	AF247164	Oryza sativa alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
AAB37749.1	U30460	Cucumis sativus expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAG32920.1	AF184232	Lycopersicon esculentum expansin. Exp8.
CAC06433.1	AJ276007	Festuca pratensis expansin. exp2.
AAF62181.1	AF247163	Oryza sativa alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAC96079.1	AF049352	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
AAC96077.1	AF049350	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
BAA88200.1	AP000837	Oryza sativa EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAF17571.1	AF202120	Regnellidium diphyllum alpha-expansin. EXP1. Rd-EXP1.
AAC96078.1	AF049351	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAG01874.1	AF291658	Striga asiatica alpha-expansin 2. Exp2.

SEQ ID NO: 634

AAF63205.1	AF245119	Mesembryanthemum crystallinum AP2-related transcription factor. CDBP. stress induced transcription factor.
BAA97122.1	AB016264	Nicotiana sylvestris ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
BAA07321.1	D38123	Nicotiana tabacum ERF1. ethylene-responsive transcription factor.
AAG43545.1	AF211527	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
BAA87068.1	AB035270	Matricaria chamomilla ethylene-responsive element binding protein1 homolog. McEREBP1.
BAA97124.1	AB016266	Nicotiana sylvestris ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
AAC62619.1	AF057373	Nicotiana tabacum transcription factor. ethylene response element binding protein 1. EREBP1.
CAB93940.1	AJ238740	Catharanthus roseus putative transcription factor. AP2-domain DNA-binding protein. orca2.

AAK31279.1 AC079890 *Oryza sativa*  
putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

AAG60182.1 AC084763 *Oryza sativa*  
putative ethylene-responsive element binding protein. OSJNBB0027P10.12.

CAB96900.1 AJ251250 *Catharanthus roseus*  
transcription factor. AP2-domain DNA-binding protein. orca3.

CAB96899.1 AJ251249 *Catharanthus roseus*  
transcription factor. AP2-domain DNA-binding protein. orca3.

CAC12822.1 AJ299252 *Nicotiana tabacum*  
AP2 domain-containing transcription factor. ap2.

AAF23899.1 AF193803 *Oryza sativa*  
transcription factor EREBP1. EREBP/AP2-like transcription factor.

AAF05606.1 AF190770 *Oryza sativa*  
EREBP-like protein. tsh1. TSH1; induced by ethylene.

BAA97123.1 AB016265 *Nicotiana sylvestris*  
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.

BAA76734.1 AB024575 *Nicotiana tabacum*  
ethylene responsive element binding factor.

BAB03248.1 AB037183 *Oryza sativa*  
ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.

CAB93939.1 AJ238739 *Catharanthus roseus*  
putative transcription factor. AP2-domain DNA-binding protein. orca1.

AAD00708.1 U91857 *Stylosanthes hamata*  
ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

AAG43548.1 AF211530 *Nicotiana tabacum*  
Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

AAG43549.1 AF211531 *Nicotiana tabacum*  
Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.

AAK31271.1 AC079890 *Oryza sativa*  
putative transcriptional factor. OSJNBb0089A17.22.

AAK01088.1 AF298230 *Hordeum vulgare*  
CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.

AAC49567.1 U41466 *Zea mays*  
Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the *Arabidopsis* floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.

SEQ ID NO: 635

CAC19789.1 AJ251686 *Catharanthus roseus*  
putative transcription factor. MYB-like DNA-binding protein. bpf-1.

CAA55693.1 X79086 Zea mays  
initiator-binding protein. IBP2.

CAA55691.1 X79085 Zea mays  
initiator binding protein. IBP1.

AAF97508.1 AF242298 Oryza sativa  
telomere binding protein-1. TBP1.

SEQ ID NO: 636

CAB43505.1 AJ239051 Cicer arietinum  
cytochrome P450. cyp81E2.

BAA22422.1 AB001379 Glycyrrhiza echinata  
cytochrome P450. CYP81E1.

BAA74465.1 AB022732 Glycyrrhiza echinata  
cytochrome P450. CYP Ge-31.

CAA10067.1 AJ012581 Cicer arietinum  
cytochrome P450. cyp81E3.

CAB41490.1 AJ238439 Cicer arietinum  
cytochrome P450 monooxygenase. cyp81E3v2.

BAA93634.1 AB025016 Lotus japonicus  
cytochrome P450.

CAA04117.1 AJ000478 Helianthus tuberosus  
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-race).

CAA04116.1 AJ000477 Helianthus tuberosus  
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

AAK38080.1 AF321856 Lolium rigidum  
putative cytochrome P450.

AAK38079.1 AF321855 Lolium rigidum  
putative cytochrome P450.

AAK38081.1 AF321857 Lolium rigidum  
putative cytochrome P450.

AAC34853.1 AF082028 Hemerocallis hybrid cultivar  
putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3.  
mRNA accumulates in senescing petals.

CAA65580.1 X96784 Nicotiana tabacum  
cytochrome P450. hsr515.

CAB56742.1 AJ249800 Cicer arietinum  
cytochrome P450 monooxygenase. cyp81E5.

AAA32913.1 M32885 Persea americana  
cytochrome P-450LXXIA1 (cyp71A1).

BAA12159.1 D83968 Glycine max  
Cytochrome P-450 (CYP93A1).

AAD56282.1 AF155332 Petunia x hybrida  
flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

CAA71515.1 Y10491 Glycine max  
putative cytochrome P450.

AAB94590.1 AF022461 Glycine max  
CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.

CAA71516.1 Y10492 Glycine max  
putative cytochrome P450.

CAA64635.1 X95342 Nicotiana tabacum  
cytochrome P450. hsr515. hypersensitivity-related gene.

BAA13076.1 D86351 Glycine max  
cytochrome P-450 (CYP93A2).

AAG44132.1 AF218296 Pisum sativum  
cytochrome P450. P450 isolog.

AAG09208.1 AF175278 Pisum sativum  
wound-inducible P450 hydroxylase. CYP82A1.

AAC49188.2 U29333 Pisum sativum  
cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.

AAD38930.1 AF135485 Glycine max  
cytochrome P450 monooxygenaseCYP93D1. CYP93E1.

CAA71876.1 Y10982 Glycine max  
putative cytochrome P450.

CAA70575.1 Y09423 Nepeta racemosa  
cytochrome P450. CYP71A5.

CAA70576.1 Y09424 Nepeta racemosa  
cytochrome P450. CYP71A6.

CAA71513.1 Y10489 Glycine max  
putative cytochrome P450.

CAA71877.1 Y10983 Glycine max  
putative cytochrome P450.

AAB94587.1 AF022458 Glycine max  
CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

AAC39454.1 AF014802 Eschscholzia californica  
(S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of Pisum sativum GenBank Accession Number U29333.

BAA92894.1 AB006790 Petunia x hybrida  
cytochrome P450. IMT-2.

BAA84072.1 AB028152 Torenia hybrida  
flavone synthase II. cytochrome P450. TFNS5.

BAA35080.1 AB015762 Nicotiana tabacum  
putative cytochrome P450. CYP82E1.

CAB56743.1 AJ249801 Cicer arietinum  
cytochrome P450 monooxygenase. cyp81E4.

AAB17562.1 U72654 *Eustoma grandiflorum*  
flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

AAG34695.1 AF313492 *Matthiola incana*  
putative cytochrome P450.

BAA74466.1 AB022733 *Glycyrrhiza echinata*  
cytochrome P450. CYP Ge-51.

BAA22423.1 AB001380 *Glycyrrhiza echinata*  
cytochrome P450. CYP93B1.

SEQ ID NO: 639

AAC06319.1 AF053084 *Malus x domestica*  
putative cinnamyl alcohol dehydrogenase. CAD.

CAA61275.1 X88797 *Eucalyptus gunnii*  
cinnamyl alcohol dehydrogenase. CAD1.

SEQ ID NO: 640

BAA92916.1 AP001539 *Oryza sativa*  
EST C26826(C50159) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC F13A10; putative ARF1 family auxin responsive transcription factor. (AC006418).

AAK21342.1 AC024594 *Oryza sativa*  
putative transcription factor. OSJNBA0093B11.2.

AAG43286.1 AF140228 *Oryza sativa*  
auxin response factor 1.

SEQ ID NO: 641

CAC24691.1 AJ132363 *Brassica juncea*  
efflux carrier of polar auxin transport. pina.

AAG17172.1 AF190881 *Populus tremula x Populus tremuloides*  
PIN1-like auxin transport protein. ppl1.

AAC39514.1 AF056027 *Oryza sativa*  
auxin transport protein REH1. REH1. potential membrane protein.

SEQ ID NO: 642

AAG22044.1 AF305783 *Pisum sativum*  
apyrase 2. apy2. phosphatase.

AAF00610.1 AF156781 *Dolichos biflorus*  
apyrase. apyrase-2.

AAG32959.1 AF207687 *Glycine soja*  
apyrase GS50.

AAG32960.1 AF207688 *Glycine soja*  
apyrase GS52.

AAF00609.1 AF156780 *Lotus japonicus*  
apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

AAD31285.1 AF139807 *Dolichos biflorus*  
apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

AAF00611.1	AF156782	Medicago sativa apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
AAK15160.1	AF288132	Medicago truncatula putative apyrase. apy1. nucleotide phosphohydrolase; Mtapy1.
BAB18896.1	AB038669	Pisum sativum apyrase.
BAB18895.1	AB038668	Pisum sativum apyrase.
BAB18894.1	AB038555	Pisum sativum apyrase H-type.
BAB18893.1	AB038554	Pisum sativum apyrase S-type.
BAB18900.1	AB027614	Pisum sativum apyrase.
BAB40230.1	AB027613	Pisum sativum S-type apyras. ATP diphosphohydrolase (apyrase) S-type.
BAB18890.1	AB023621	Pisum sativum apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.
BAA75506.1	AB022319	Pisum sativum apyrase. cytoskeleton associated.
BAA89275.1	AB027616	Pisum sativum apyrase.
BAB40231.1	AB027615	Pisum sativum S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
AAB02720.1	U58597	Solanum tuberosum catalyzes the hydrolysis of phosphoanhydride bonds of nucleoside tri- and di- phosphates in the presence of divalent cations. ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-type ATPase; NTP-diphosphohydrolase.
AAK15161.1	AF288133	Medicago truncatula putative apyrase. apy4. nucleotide phosphohydrolase; Mtapy4.
BAB18891.1	AB030444	Pisum sativum apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence is reported in Acc#:AB022319.
BAB18892.1	AB030445	Pisum sativum apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is reported in Acc#:AB022319, Acc#:AB027613.
SEQ ID NO: 645		
AAG22044.1	AF305783	Pisum sativum apyrase 2. apy2. phosphatase.
AAF00610.1	AF156781	Dolichos biflorus apyrase. apyrase-2.
AAG32959.1	AF207687	Glycine soja apyrase GS50.

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AAG32960.1 AF207688 Glycine soja  
apyrase GS52.

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AAD31285.1 AF139807 Dolichos biflorus  
apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

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AAK15160.1 AF288132 Medicago truncatula  
putative apyrase. apy1. nucleotide phosphohydrolase; Mtapy1.

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AAF00609.1 AF156780 Lotus japonicus  
apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

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BAB18896.1 AB038669 Pisum sativum  
apyrase.

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BAB18895.1 AB038668 Pisum sativum  
apyrase.

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BAB18894.1 AB038555 Pisum sativum  
apyrase H-type.

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BAB18893.1 AB038554 Pisum sativum  
apyrase S-type.

---

BAB18900.1 AB027614 Pisum sativum  
apyrase.

---

BAB40230.1 AB027613 Pisum sativum  
S-type apyras. ATP diphosphohydrolase (apyrase) S-type.

---

BAB18890.1 AB023621 Pisum sativum  
apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.

---

BAA75506.1 AB022319 Pisum sativum  
apyrase. cytoskeleton associated.

---

AAF00611.1 AF156782 Medicago sativa  
apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

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BAA89275.1 AB027616 Pisum sativum  
apyrase.

---

BAB40231.1 AB027615 Pisum sativum  
S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.

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AAB02720.1 U58597 Solanum tuberosum  
catalyzes the hydrolysis of phosphoanhydride bonds of nucleoside tri- and di- phosphates in  
the presence of divalent cations. ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-  
type ATPase; NTP-diphosphohydrolase.

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AAK15161.1 AF288133 Medicago truncatula  
putative apyrase. apy4. nucleotide phosphohydrolase; Mtapy4.

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BAB18891.1 AB030444 Pisum sativum  
apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence is reported in Acc#:AB022319.

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BAB18892.1 AB030445 Pisum sativum  
apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is reported in Acc#:AB022319,  
Acc#:AB027613.

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SEQ ID NO: 646

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AAB80947.1 AF022915 *Triticum aestivum*  
ornithine/acetylornithine aminotransferase.

CAA69936.1 Y08680 *Alnus glutinosa*  
acetylornithine aminotransferase. ag118.

AAK11219.1 AF324485 *Oryza sativa*  
aminotransferase-like protein.

AAG09278.1 AF177590 *Vitis vinifera*  
ornithine aminotransferase.

AAC78480.1 AF085149 *Capsicum chinense*  
putative aminotransferase. pyridoxal phosphate dependent.

AAA02916.1 L08400 *Vigna aconitifolia*  
production of pyrroline-5-carboxylate by deamination of ornithine. ornithine aminotransferase.

AAB59330.1 M31545 *Hordeum vulgare*  
glutamate 1-semialdehyde aminotransferase. GSA. precursor.

AAA18861.1 U03632 *Chlamydomonas reinhardtii*  
glutamate-1-semialdehyde aminotransferase. gsa.

AAA33968.1 L12453 *Glycine max*  
catalyzes 5-aminolevulinic acid formation from GSA. glutamate 1-semialdehyde aminotransferase. Gsa. putative.

AAC48996.1 U20260 *Glycine max*  
converts GSA to 5-aminolevulinic acid. glutamate 1-semialdehyde aminotransferase. Gsa1.

SEQ ID NO: 650

AAF66982.1 AF247646 *Zea mays*  
transposase. similar to Mutator family transposases.

SEQ ID NO: 652

AAB41812.1 L36158 *Medicago sativa*  
peroxidase. pxdD. amino acid feature: conserved domains, aa 120 .. 126, 188 .. 195; amino acid feature: heme-binding domain, aa 63 .. 68.

CAA71495.1 Y10469 *Spinacia oleracea*  
peroxidase. prxr8.

CAA09881.1 AJ011939 *Trifolium repens*  
peroxidase. prx2.

CAA62228.1 X90695 *Medicago sativa*  
peroxidase2. prx2.

AAA98491.1 L36981 *Petroselinum crispum*  
anionic peroxidase.

BAB39281.1 AP002971 *Oryza sativa*  
putative peroxidase. P0537A05.10. contains ESTs D24657(R2329),AU082066(R2329).

AAB02926.1 U59284 *Linum usitatissimum*  
peroxidase. FLXPER3.

BAA77387.1 AB024437 *Scutellaria baicalensis*  
peroxidase 1.

CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA71488.1	Y10462	Spinacia oleracea peroxidase. prxr1.
BAA01950.1	D11337	Vigna angularis peroxidase.
BAA14143.1	D90115	Armoracia rusticana peroxidase isozyme.
CAA71490.1	Y10464	Spinacia oleracea peroxidase. prxr3.
CAB94692.1	AJ242742	Ipomoea batatas Removal of H <sub>2</sub> O <sub>2</sub> , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
BAA92497.1	AP001383	Oryza sativa ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to peroxidase ATP18a. (X98804).
AAC36707.1	AF078691	Manihot esculenta peroxidase.
BAA92422.1	AP001366	Oryza sativa ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to A.thaliana mRNA for peroxidase ATP18a. (X98804).
CAA62226.1	X90693	Medicago sativa peroxidase1B. prx1B.
AAF63024.1	AF244921	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
AAA32676.1	M37637	Arachis hypogaea cationic peroxidase. PNC2.
BAA11853.1	D83225	Populus nigra peroxidase.
CAC21393.1	AJ401276	Zea mays peroxidase. pox3.
AAA65636.1	L13653	Lycopersicon esculentum peroxidase. TPX2.
CAB67121.1	Y19023	Lycopersicon esculentum peroxidase. cevi-1.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
CAA50597.1	X71593	Lycopersicon esculentum peroxidase. CEVI-1.
AAD37376.1	AF145350	Glycine max peroxidase. Prx4.
AAB67737.1	L77080	Stylosanthes humilis cationic peroxidase.

CAA71489.1	Y10463	Spinacia oleracea
peroxidase. prxr2.		
CAA71496.1	Y10470	Spinacia oleracea
peroxidase. prxr9.		
CAA71494.1	Y10468	Spinacia oleracea
peroxidase. prxr7.		
BAA06334.1	D30652	Populus kitakamiensis
peroxidase.		
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa
signal for ER. peroxidase.		
BAA94962.1	AB042103	Asparagus officinalis
peroxidase. AspPOX1.		
CAA80502.1	Z22920	Spirodela polyrrhiza
peroxidase.		
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa
signal for ER. peroxidase.		
BAA11852.1	D83224	Populus nigra
peroxidase.		
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa
signal for ER. peroxidase.		
BAA07241.1	D38051	Populus kitakamiensis
peroxidase. prxA4a.		
AAD11481.1	U51191	Glycine max
peroxidase precursor. sEPa1.		
AAC98519.1	AF007211	Glycine max
peroxidase precursor. GMIPER1. pathogen-induced.		
AAA32973.1	M73234	Hordeum vulgare
peroxidase BP 1. Prx5.		
AAB47602.1	L07554	Linum usitatissimum
peroxidase. FLXPER1.		
AAB41810.1	L36156	Medicago sativa
peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.		
AAF63027.1	AF244924	Spinacia oleracea
hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.		
AAA34108.1	J02979	Nicotiana tabacum
lignin-forming peroxidase precursor (EC 1.11.1.7).		
AAD43561.1	AF155124	Gossypium hirsutum
bacterial-induced peroxidase precursor. Perx_Goshiko.		
SEQ ID NO: 653		

AAB97617.1	U83687	Apium graveolens NADPH-dependent mannose 6-phosphate reductase. m6pr. aldo-keto reductase; similar to aldose 6-phosphate reductase also known as NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession Number D11080.
BAA01853.1	D11080	Malus x domestica NADP-dependent D-sorbitol-6-phosphate dehydrogenase. S6PDH.
AAC97607.1	AF057134	Malus x domestica synthesizes sorbitol, a major photosynthetic product in many members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate dehydrogenase. S6PDH.
SEQ ID NO: 654		
BAA82556.1	AB030083	Populus nigra lectin-like protein kinase. PnLPK.
AAB61708.1	U93048	Daucus carota somatic embryogenesis receptor-like kinase. SERK.
BAB19337.1	AP003044	Oryza sativa putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
AAD21872.1	AF078082	Phaseolus vulgaris receptor-like protein kinase homolog RK20-1.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.
CAB51480.1	Y14600	Sorghum bicolor putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
AAG59657.1	AC084319	Oryza sativa putative protein kinase. OSJNBa0004B24.20.
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

CAB51834.1	00069	Oryza sativa
11332.5. contains eukaryotic protein kinase domain PF.		
BAA94509.1	AB041503	Populus nigra
protein kinase 1. PnPK1.		
AAG16628.1	AY007545	Brassica napus
protein serine/threonine kinase BNK1.		
BAA87853.1	AP000816	Oryza sativa
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).		
BAB03429.1	AP002817	Oryza sativa
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).		
BAB07999.1	AP002525	Oryza sativa
putative protein kinase. P0462H08.22. contains EST C22619(S11214).		
BAB21240.1	AP002953	Oryza sativa
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).		
BAA92954.1	AP001551	Oryza sativa
Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).		
BAA94510.1	AB041504	Populus nigra
protein kinase 2. PnPK2.		
AAG03090.1	AC073405	Oryza sativa
Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).		
AAF91322.1	AF244888	Glycine max
receptor-like protein kinase 1. RLK1. GmRLK1.		
BAA94517.1	AP001800	Oryza sativa
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).		
BAB07905.1	AP002835	Oryza sativa
putative S-receptor kinase. P0417G05.13.		
CAB51836.1	AJ243961	Oryza sativa
Putitive Ser/Thr protein kinase. 11332.7.		
BAA78764.1	AB023482	Oryza sativa
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).		
AAA33915.1	L27821	Oryza sativa
receptor type serine/threonine kinase. protein kinase.		
AAF91323.1	AF244889	Glycine max
receptor-like protein kinase 2. RLK2. GmRLK2.		
CAA67145.1	X98520	Brassica oleracea
receptor-like kinase. SFR2.		
CAA73133.1	Y12530	Brassica oleracea
serine /threonine kinase. ARLK.		
AAF91324.1	AF244890	Glycine max
receptor-like protein kinase 3. RLK3. GmRLK3.		

CAA74661.1	Y14285	Brassica oleracea
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.		
BAA92953.1	AP001551	Oryza sativa
Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).		
BAB40094.1	AP003210	Oryza sativa
putative receptor protein kinase. OSJNBA0010K01.7.		
AAF43496.1	AF131222	Lophopyrum elongatum
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.		
AAK11674.1	AF339747	Lophopyrum elongatum
protein kinase. ESI47.		
BAB07906.1	AP002835	Oryza sativa
putative S-receptor kinase. P0417G05.14.		
BAA94516.1	AP001800	Oryza sativa
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).		
CAB41878.1	Y18259	Brassica oleracea
SRK5 protein. SRK5. receptor-like kinase.		
BAA23676.1	AB000970	Brassica rapa
receptor kinase 1. BcRK1.		
CAB41879.1	Y18260	Brassica oleracea
SRK15 protein. SRK15. receptor-like kinase.		
SEQ ID NO: 655		
AAD21872.1	AF078082	Phaseolus vulgaris
receptor-like protein kinase homolog RK20-1.		
CAA73134.1	Y12531	Brassica oleracea
serine/threonine kinase. BRLK.		
CAA67145.1	X98520	Brassica oleracea
receptor-like kinase. SFR2.		
CAA73133.1	Y12530	Brassica oleracea
serine /threonine kinase. ARLK.		
AAB93834.1	U82481	Zea mays
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.		
BAA23676.1	AB000970	Brassica rapa
receptor kinase 1. BcRK1.		
AAC23542.1	U20948	Ipomoea trifida
receptor protein kinase. IRK1.		
CAB41879.1	Y18260	Brassica oleracea
SRK15 protein. SRK15. receptor-like kinase.		

CAA74662.1 Y14286 *Brassica oleracea*  
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

CAB89179.1 AJ245479 *Brassica napus* subsp. *napus*  
ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 *Brassica napus*  
serine/threonine kinase receptor.

AAA62232.1 U00443 *Brassica napus*  
S-receptor kinase. protein contains an immunoglobulin-like domain.

CAA74661.1 Y14285 *Brassica oleracea*  
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

AAA33000.1 M76647 *Brassica oleracea*  
receptor protein kinase. SKR6.

CAA79355.1 Z18921 *Brassica oleracea*  
S-receptor kinase-like protein.

CAB41878.1 Y18259 *Brassica oleracea*  
SRK5 protein. SRK5. receptor-like kinase.

BAA07576.1 D38563 *Brassica rapa*  
receptor protein kinase SRK8.

BAA06285.1 D30049 *Brassica rapa*  
S-receptor kinase SRK9.

BAA21132.1 D88193 *Brassica rapa*  
S-receptor kinase. SRK9 (B.c.).

BAA07577.2 D38564 *Brassica rapa*  
receptor protein kinase SRK12.

BAA92836.1 AB032473 *Brassica oleracea*  
S18 S-locus receptor kinase. SRK18.

BAB21001.1 AB054061 *Brassica rapa*  
S locus receptor kinase. SRK22.

BAA92837.1 AB032474 *Brassica oleracea*  
S60 S-locus receptor kinase. SRK60.

BAB18292.1 AP002860 *Oryza sativa*  
putative receptor-like protein kinase. P0409B08.19.

AAD52097.1 AF088885 *Nicotiana tabacum*  
receptor-like kinase CHRK1. Chrk1.

BAB39873.1 AP002882 *Oryza sativa*  
putative protein kinase. P0439B06.8. contains ESTs  
AU056701(S20808),AU056702(S20808).

AAK21965.1 AY028699 *Brassica napus*  
receptor protein kinase PERK1.

AAA33915.1 L27821 *Oryza sativa*  
receptor type serine/threonine kinase. protein kinase.

AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBA0071K19.11.
BAA94529.2	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAF34428.1	AF172282	Oryza sativa receptor-like protein kinase. DUPR11.18.
AAG03090.1	AC073405	Oryza sativa Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA94516.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.13.
BAB07906.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.14.
SEQ ID NO: 657		
AAF43869.1	AF166114	Chloroplast Mesostigma viride probable transport protein. cysA.
BAB17113.1	AP002866	Oryza sativa putative white protein; ATP-binding cassette transporter. P0410E01.34.
BAA57907.1	AB001684	Chlorella vulgaris sulfate transport system permease protein. cysA.
AAD54843.1	AF137379	Chloroplast Nephroselmis olivacea probable transport protein. cysA.
BAA90508.1	AP001111	Oryza sativa similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA90507.1	AP001111	Oryza sativa similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA83352.1	AP000391	Oryza sativa ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
AAG49003.1	AY013246	Hordeum vulgare putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAD10836.1	U52079	Solanum tuberosum P-glycoprotein. pmdr1. binds ATP; ATPase; transporter; transmembrane protein.

BAA96612.1 AP002482 Oryza sativa  
 Similar to *Arabidopsis thaliana* chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411).

BAB40032.1 AP003046 Oryza sativa  
 putative ABC transporter. P0445D12.3.

AAG45492.1 AY013245 Oryza sativa  
 36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.

AAG49002.1 AY013246 Hordeum vulgare  
 putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.

BAB21275.1 AP002844 Oryza sativa  
 putative ABC transporter protein. P0410E03.6.

BAB21273.1 AP002844 Oryza sativa  
 putative ABC transporter protein. P0410E03.4.

CAA94437.1 Z70524 Spirodela polyrrhiza  
 multidrug resistance protein. PDR5-like ABC transporter.

BAB21276.1 AP002844 Oryza sativa  
 putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).

BAB21279.1 AP002844 Oryza sativa  
 putative ABC transporter protein. P0410E03.10. contains ESTs  
 AU065360(R3463),AU101680(R3463).

SEQ ID NO: 658

AAD10386.1 U72255 Oryza sativa  
 beta-1,3-glucanase precursor. Gns9.

BAA89481.1 AB029462 Salix gilgiana  
 beta-1,3-glucanase. SgGN1.

CAB85903.1 AJ251646 Pisum sativum  
 hydrolysis of beta-1,3 conjugated glucans. beta-1,3 glucanase. gns2.

CAA49513.1 X69887 Brassica napus  
 beta-1,3-glucanase homologue.

AAA90953.1 U30323 Triticum aestivum  
 beta 1,3-glucanase. Glc1.

BAB19363.1 AP002542 Oryza sativa  
 putative beta-1,3-glucanase. P0679C08.2.

CAA82271.1 Z28697 Nicotiana tabacum  
 beta-1,3-glucanase.

CAA30261.1 X07280 Nicotiana plumbaginifolia  
 beta-glucanase.

AAA51643.1 M23120 Nicotiana plumbaginifolia  
 beta-glucanase precursor.

AAA34078.1 M63634 Nicotiana plumbaginifolia  
 regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.

AAB82772.2	AF001523	Musa acuminata beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
AAF08679.1	AF004838	Musa acuminata beta-1,3-glucanase.
CAB71021.1	AJ271598	Hieracium piloselloides putative role in callose degradation. putative beta-1,3-glucanase. gluc.
AAD10383.1	U72252	Oryza sativa beta-1,3-glucanase precursor. Gns6.
AAD28732.1	AF112965	Triticum aestivum beta-1,3-glucanase precursor. Glb3.
BAB40807.1	AB052291	Pyrus pyrifolia catalyzing the hydrolysis of 1,3-beta-glucosyl linkages. endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the protein(BGN-1) encoded by pear pollen bgn-1 with barley endo-1,3-beta-glucanase(GII. accession number: pdb/1GHS-B/2.3/2/306/N/)(40% identity) and their hydrophobic cluster analysis(HCA)(a overall HCA homology score of 87.1%) showed that it was most likely that the bgn-1 encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession number: dad/AJ251646-1).
AAA63539.1	M60402	Nicotiana tabacum glucan beta-1,3-glucanase. glucanase GLA.
AAA63541.1	M59442	Nicotiana tabacum basic beta-1,3-glucanase. glucanase.
AAA63540.1	M60403	Nicotiana tabacum glucan-1,3-beta-glucosidase. glucanase GLB.
AAA32939.1	M62907	Hordeum vulgare hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase. cBGL32.
AAC14399.1	AF030771	Hordeum vulgare beta-1,3-glucanase 2. BGL32.
AAA87456.1	U22147	Hevea brasiliensis beta-1,3-glucanase. HGN1. hydrolytic enzyme.
BAA77784.1	AB027429	Oryza sativa beta-1,3-glucanase.
BAA77785.1	AB027430	Oryza sativa beta-1,3-glucanase.
CAB91554.1	AJ277900	Vitis vinifera beta 1-3 glucanase. g1.
AAD10381.1	U72250	Oryza sativa beta-1,3-glucanase precursor. Gns4.
AAA33946.1	M37753	Glycine max beta-1,3-endoglucanase (EC 3.2.1.39).
AAD33881.1	AF141654	Nicotiana tabacum beta-1,3-glucanase. GGL4.

AAB86541.1	AF030166	Oryza sativa glucanase. glu1.
AAD10384.1	U72253	Oryza sativa beta-1,3-glucanase precursor. Gns7.
CAB38443.1	AJ133470	Hevea brasiliensis beta-1,3-glucanase. hgn1.
AAB03501.1	U41323	Glycine max beta-1,3-glucanase. SGN1.
AAA18928.1	U01901	Solanum tuberosum catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA88794.1	U01900	Solanum tuberosum catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB1. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAC19114.1	AF067863	Solanum tuberosum 1,3-beta-glucan glucanohydrolase. glucanase.
AAG24921.1	AF311749	Hevea brasiliensis beta-1,3-glucanase.
CAA03908.1	AJ000081	Citrus sinensis glucan hydrolase. beta-1,3-glucanase. gns1.
CAA37289.1	X53129	Phaseolus vulgaris 1,3-beta-D-glucanase.
CAA57255.1	X81560	Nicotiana tabacum (1-)beta-glucanase. Sp41a.

SEQ ID NO: 659

AAB65776.1	U97521	Vitis vinifera class IV endochitinase. VvChi4A.
AAB65777.1	U97522	Vitis vinifera class IV endochitinase. VvChi4B.
BAA03751.1	D16223	Oryza sativa endochitinase. Cht-3.
CAA30142.1	X07130	Solanum tuberosum endochitinase.
BAA03749.1	D16221	Oryza sativa endochitinase. Cht-1.

SEQ ID NO: 660

AAF07221.1	AF072519	Nicotiana tabacum centrin. CEN1. caltractin; EF-hand domain calcium-binding protein.
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AAF07222.1	AF072520	Nicotiana tabacum centrin. CEN2. caltractin; EF-hand domain calcium-binding protein.
CAA49153.1	X69220	Scherffelia dubia caltractin.
AAC04626.1	U92973	Marsilea vestita calcium-binding protein. centrin. MvCen1. caltractin.
AAB67855.1	U53812	Dunaliella salina caltractin-like protein.
CAA41039.1	X57973	Chlamydomonas reinhardtii caltractin.
CAA31163.1	X12634	Chlamydomonas reinhardtii caltractin (AA 1 - 169).
SEQ ID NO: 664		
BAB16432.1	AB041520	Nicotiana tabacum WRKY transcription factor Nt-SubD48. Nt-SubD48.
AAC49528.1	U56834	Petroselinum crispum DNA-binding. WRKY3. WRKY-type DNA-binding protein.
AAD27591.1	AF121354	Petroselinum crispum binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
AAD32676.1	AF140553	Avena sativa DNA-binding protein WRKY3. wrky3. putative transcription factor.
BAA77358.1	AB020023	Nicotiana tabacum WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG46150.1	AC018727	Oryza sativa putative DNA-binding protein. OSJNBa0056G17.18.
BAB40073.1	AP003074	Oryza sativa putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
BAB18313.1	AP002865	Oryza sativa putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
AAD38283.1	AC007789	Oryza sativa putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAA77383.1	AB020590	Nicotiana tabacum transcription factor NtWRKY2.
BAA82107.1	AB022693	Nicotiana tabacum transcription factor. NtWRKY1.
CAA88326.1	Z48429	Avena satua binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD32677.1	AF140554	Avena sativa DNA-binding protein WRKY1. wrky1. putative transcription factor.
AAD55974.1	AF121353	Petroselinum crispum zinc-finger type transcription factor WRKY1. WRKY1.

AAC49529.1	U58540	Petroselinum crispum
WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.		
AAC49527.1	U48831	Petroselinum crispum
WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.		
AAC31956.1	AF080595	Pimpinella brachycarpa
zinc finger protein. ZFP1. WRKY1.		
BAA86031.1	AB026890	Nicotiana tabacum
transcription factor NtWRKY4.		
AAD16139.1	AF096299	Nicotiana tabacum
DNA-binding protein 2. WRKY2. transcription factor.		
AAF23898.1	AF193802	Oryza sativa
zinc finger transcription factor WRKY1.		
AAD16138.1	AF096298	Nicotiana tabacum
DNA-binding protein 1. WRKY1. transcription factor.		
AAC37515.1	L44134	Cucumis sativus
SPF1-like DNA-binding protein.		
AAG35658.1	AF204925	Petroselinum crispum
transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.		
CAA88331.1	Z48431	Avena fatua
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.		
BAB19075.1	AP002744	Oryza sativa
putative DNA-binding protein homolog. P0006C01.17.		
BAB19096.1	AP002839	Oryza sativa
putative DNA-binding protein homolog. P0688A04.2.		
AAK16170.1	AC079887	Oryza sativa
putative DNA binding protein. OSJNBa0040E01.4.		
AAK16171.1	AC079887	Oryza sativa
putative DNA-binding protein. OSJNBa0040E01.10.		
AAG35659.1	AF204926	Petroselinum crispum
transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.		
CAB97004.1	AJ278507	Solanum tuberosum
putative transcription factor. WRKY DNA binding protein. WRKY1.		
AAF61864.1	AF193771	Nicotiana tabacum
DNA-binding protein 4. WRKY4. transcription factor.		
BAA87069.1	AB035271	Matricaria chamomilla
elicitor-induced DNA-binding protein homolog. McWRKY1.		
AAF61863.1	AF193770	Nicotiana tabacum
DNA-binding protein 3. WRKY3. transcription factor.		
SEQ ID NO: 665		
AAD02558.1	AF049933	Petunia x hybrida
PGPS/NH17. PGPS/NH17. protein sec61 gamma subunit homolog; protein transport to ER.		
SEQ ID NO: 667		

AAD51623.1 AF169020 Glycine max  
 seed maturation protein PM35. PM35. similar to Phaseolus vulgaris putative osmoprotector PvLEA-18.

AAC49859.1 U72764 Phaseolus vulgaris  
 putative osmoprotector. PvLEA-18. Pvlea-18. atypical late embryogenesis abundant protein.

AAF81194.1 AF240774 Phaseolus vulgaris  
 LEA-18.

SEQ ID NO: 672

CAB40743.1 AJ011885 Solanum tuberosum  
 starch branching enzyme II. sbe II.

CAB40746.1 AJ011888 Solanum tuberosum  
 starch branching enzyme II. SBE II.

CAB40748.1 AJ011890 Solanum tuberosum  
 starch branching enzyme II. SBE II.

AAD30186.1 AF076679 Triticum aestivum  
 starch branching enzyme-I. SBE-I.

AAD30187.1 AF076680 Aegilops tauschii  
 starch branching enzyme-I. SBE-I.

BAA82348.1 AB029548 Phaseolus vulgaris  
 branching enzyme 1. kbe1.

CAA56319.1 X80009 Pisum sativum  
 starch branching enzyme I. SBEI.

CAB40747.1 AJ011889 Solanum tuberosum  
 starch branching enzyme II. SBE II.

CAA03846.1 AJ000004 Solanum tuberosum  
 branches 1,4-alpha glucans. starch branching enzyme II, SBE-II. Sbe-II.

BAA03738.1 D16201 Oryza sativa  
 branching enzyme-3 precursor.

AAG27623.1 AF286319 Triticum aestivum  
 starch branching enzyme 2. Sbe2. glucosyltransferase.

CAA72154.1 Y11282 Triticum aestivum  
 1,4-alpha-glucan branching enzyme II. sbe2.

AAK26821.1 AF338431 Aegilops tauschii  
 starch branching enzyme IIa. SBEIIa.

AAK26822.1 AF338432 Triticum aestivum  
 starch branching enzyme IIa variant. SBEIIa variant.

AAC33764.1 AF072725 Zea mays  
 starch branching enzyme IIb. ae. SBEIIb.

AAA18571.1 L08065 Zea mays  
 starch branching enzyme II.

BAA82828.1 AB023498 Oryza sativa  
 starch branching enzyme rbe4. RBE4.

AAC69753.1 AF064560 *Hordeum vulgare*  
starch branching enzyme IIa. sbeIIa.

CAA56320.1 X80010 *Pisum sativum*  
starch branching enzyme II. SBEII.

AAC69754.1 AF064561 *Hordeum vulgare*  
starch branching enzyme IIb. sbeIIb.

AAC36471.1 AF072724 *Zea mays*  
starch branching enzyme I. sbe1. confirmed by partial peptide sequencing.

AAA82735.1 U17897 *Zea mays*  
starch branching enzyme I. sbe1.

AAD50279.2 AF169833 *Sorghum bicolor*  
seed starch branching enzyme. SBE.

BAA01854.1 D11081 *Zea mays*  
branching enzyme-I precursor.

CAA49463.1 X69805 *Solanum tuberosum*  
1,4-alpha-glucan branching enzyme. SBE.

CAA70038.1 Y08786 *Solanum tuberosum*  
1,4-alpha-glucan branching enzyme. sbeI.

AAB17086.1 U66376 *Triticum aestivum*  
1,4-alpha-D-glucan 6-alpha-D-(1,4-alpha-D-glucanotransferase. branching enzyme.

AAB67316.1 U65948 *Zea mays*  
formation of alpha-1-6 glucosidic linkage in starch biosynthesis. starch branching enzyme IIa. Sbe2a. starch branching enzyme isozyme SBEIIa.

BAB40334.1 AB042937 *Ipomoea batatas*  
starch branching enzyme. IBE.

BAA01584.1 D10752 *Oryza sativa*  
branching enzyme.

AAD28284.1 AF136268 *Oryza sativa* subsp. *japonica*  
starch-branching enzyme I. Rbe1.

BAA01616.1 D10838 *Oryza sativa*  
1,4-alpha-glucan branching enzyme. sbe1.

BAA01855.1 D11082 *Oryza sativa*  
branching enzyme-I precursor.

CAB40981.1 AJ237897 *Triticum aestivum*  
starch branching enzyme I. sbe1. alternative.

CAB40979.1 AJ237897 *Triticum aestivum*  
starch branching enzyme I. sbe1.

CAB40980.1 AJ237897 *Triticum aestivum*  
starch branching enzyme I. sbe1. alternative.

AAG27622.1 AF286318 *Triticum aestivum*  
starch branching enzyme I. Sbe1A. glucosyltransferase.

CAA54308.1 X77012 *Manihot esculenta*  
1,4-alpha-glucan branching enzyme. SBE.

CAA72987.1 Y12320 *Triticum aestivum*  
starch branching enzyme I. Sbe1.

AAG27621.1 AF286317 *Triticum aestivum*  
starch branching enzyme I. Sbe1D. glucosyltransferase.

BAAS2349.1 AB029549 *Phaseolus vulgaris*  
branching enzyme 3. kbe3.

AAB61925.1 AF002820 *Triticum aestivum*  
starch branching enzyme I. wSBE I-D2.

CAB40749.1 AJ011891 *Solanum tuberosum*  
starch branching enzyme II. SBE II.

CAB40745.1 AJ011887 *Solanum tuberosum*  
starch branching enzyme II. SBE II.

CAB40744.1 AJ011886 *Solanum tuberosum*  
starch branching enzyme II. SBE II.

BAA85762.1 AB028067 *Nicotiana tabacum*  
starch branching enzyme. SBE.

CAA49371.1 X69713 *Manihot esculenta*  
branching enzyme. r-2.

BAB40335.1 AB042940 *Ipomoea batatas*  
starch branching enzyme. IBE.

CAA49370.1 X69712 *Manihot esculenta*  
branching enzyme. r-1.

AAC72336.1 AF064563 *Hordeum vulgare*  
starch branching enzyme IIb. sbeIIb.

SEQ ID NO: 673

CAA09881.1 AJ011939 *Trifolium repens*  
peroxidase. prx2.

CAA62228.1 X90695 *Medicago sativa*  
peroxidase2. prx2.

CAA71495.1 Y10469 *Spinacia oleracea*  
peroxidase. prxr8.

AAB41812.1 L36158 *Medicago sativa*  
peroxidase. pxdD. amino acid feature: conserved domains, aa 120 .. 126, 188 .. 195; amino acid feature: heme-binding domain, aa 63 .. 68.

BAA77387.1 AB024437 *Scutellaria baicalensis*  
peroxidase 1.

AAF63024.1 AF244921 *Spinacia oleracea*  
hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.

AAD11483.1 U51193 *Glycine max*  
peroxidase. sEPb1.

AAB67737.1 L77080 *Stylosanthes humilis*  
cationic peroxidase.

BAA07663.1	D42064	Nicotiana tabacum cationic peroxidase isozyme 38K precursor.
BAA07664.1	D42065	Nicotiana tabacum cationic peroxidase isozyme 40K precursor.
CAB94692.1	AJ242742	Ipomoea batatas Removal of H2O2, oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
CAB67121.1	Y19023	Lycopersicon esculentum peroxidase. cevi-1.
CAA62226.1	X90693	Medicago sativa peroxidase1B. prx1B.
CAA50597.1	X71593	Lycopersicon esculentum peroxidase. CEVI-1.
AAD11481.1	U51191	Glycine max peroxidase precursor. sEPa1.
AAD11484.1	U51194	Glycine max peroxidase. sEPb2.
BAA82306.1	AB027752	Nicotiana tabacum peroxidase.
AAA65637.1	L13654	Lycopersicon esculentum peroxidase. TPX1.
AAD11482.1	U51192	Glycine max peroxidase precursor. sEPa2.
CAA62225.1	X90692	Medicago sativa peroxidase1A. prx1A.
AAC98519.1	AF007211	Glycine max peroxidase precursor. GMIPER1. pathogen-induced.
AAD37427.1	AF149277	Phaseolus vulgaris peroxidase 1 precursor. FBP1. secretory peroxidase.
BAA14144.1	D90116	Armoracia rusticana peroxidase isozyme.
AAA98491.1	L36981	Petroselinum crispum anionic peroxidase.
CAA71488.1	Y10462	Spinacia oleracea peroxidase. prxr1.
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA14143.1	D90115	Armoracia rusticana peroxidase isozyme.
CAA71490.1	Y10464	Spinacia oleracea peroxidase. prxr3.
AAB02554.1	L37790	Stylosanthes humilis cationic peroxidase.

CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA01877.1	D11102	Populus kitakamiensis peroxidase. prxA1.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
BAA01950.1	D11337	Vigna angularis peroxidase.
AAF65464.2	AF247700	Oryza sativa peroxidase POC1.
AAF63027.1	AF244924	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
CAC21393.1	AJ401276	Zea mays peroxidase. pox3.
CAA59487.1	X85230	Triticum aestivum peroxidase. pox4.
AAD37430.1	AF149280	Phaseolus vulgaris peroxidase 5 precursor. FBP5. secretory peroxidase.
CAA71491.1	Y10465	Spinacia oleracea peroxidase. prxr4.
AAB41811.1	L36157	Medicago sativa peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
BAA03644.1	D14997	Oryza sativa peroxidase.
AAA32676.1	M37637	Arachis hypogaea cationic peroxidase. PNC2.
CAA71494.1	Y10468	Spinacia oleracea peroxidase. prxr7.
AAA34050.1	M74103	Nicotiana sylvestris anionic peroxidase.
CAA40796.1	X57564	Armoracia rusticana peroxidase. peroxidase precursor.
SEQ ID NO: 674		
AAG31438.1	AF241793	Perilla frutescens limonene synthase.
BAA08367.1	D49368	Perilla frutescens limonene cyclase.
BAA21629.1	AB005744	Perilla frutescens catalyzing the cyclization of geranyl pyrophosphate to 1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ Acc#D49368.

AAG31437.1	AF241792	Perilla frutescens limonene synthase.
AAK06663.1	AF317695	Perilla frutescens var. frutescens limonene synthase.
AAG31435.1	AF241790	Perilla citriodora limonene synthase.
AAF65545.1	AF233894	Perilla citriodora limonene synthase.
AAD50304.1	AF175323	Mentha longifolia limonene synthase. monoterpane synthase.
AAC37366.1	L13459	Mentha spicata 4S-limonene synthase.
AAG01140.1	AF282875	Schizonepeta tenuifolia (+)-4R-limonene synthase.
AAC61260.1	AF061285	Capsicum annuum sesquiterpene cyclase. UV induced.
AAG09949.1	AF171216	Lycopersicon esculentum vetispiradiene synthase. LEVS2. sesquiterpene cyclase.
AAF74977.1	AF270425	Gossypium hirsutum (E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene synthase. cdn2. sesquiterpene cyclase.
BAA82141.1	AB023816	Solanum tuberosum vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.
BAA82092.1	AB022598	Solanum tuberosum vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.
AAF21053.1	AF212433	Capsicum annuum UV-induced sesquiterpene cyclase. SC2.
BAA82109.1	AB022720	Solanum tuberosum vetispiradiene synthase. PVS3. potato sesquiterpene cyclase; PVS3.
BAA82108.1	AB022719	Solanum tuberosum vetispiradiene synthase. PVS2. potato sesquiterpene cyclase; PVS2.
AAC12784.1	U88318	Gossypium hirsutum (E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.
AAG24640.2	AF304444	Artemisia annua sesquiterpene cyclase.
AAK15641.1	AF326117	Capsicum annuum sesquiterpene cyclase. PSC2.
CAC12731.1	AJ271792	Artemisia annua putative sesquiterpene cyclase. cASC125.
SEQ ID NO: 675		
CAA50609.1	X71609	Nicotiana tabacum ras-related GTP-binding protein.

CAA98166.1	Z73938	Lotus japonicus GTP-binding protein. RAB5A. rab5A.
CAC24477.1	AJ296336	Cichorium intybus x Cichorium endivia GTP binding protein. chi3154.
CAC24476.1	AJ296335	Cichorium intybus x Cichorium endivia GTP binding protein. chi3152.
CAB57220.1	AJ249866	Cichorium intybus x Cichorium endivia GTP binding protein. gtp2.
CAB57219.1	AJ249865	Cichorium intybus x Cichorium endivia GTP binding protein. gtp1.
CAC24475.1	AJ296334	Cichorium intybus x Cichorium endivia GTP binding protein. chi3153.
CAA46112.1	X64941	Nicotiana plumbaginifolia small GTP binding protein.
CAC24474.1	AJ296333	Cichorium intybus x Cichorium endivia GTP binding protein. chi3151.
CAC19792.1	AJ292320	Oryza sativa small GTP-binding protein, RAB family. RAB5A protein. rab5A.
AAD28731.1	AF112964	Triticum aestivum small GTP-binding protein. Sgp.
CAA98167.1	Z73939	Lotus japonicus GTP-binding protein. RAB5B. rab5B.
CAA06922.1	AJ006225	Mesembryanthemum crystallinum small GTP-binding protein. rab5B.
AAG42497.1	AF323991	Oryza sativa small GTP-binding protein RAB5B. rab5B.
BAA84717.1	AB032761	Oryza sativa GTP-binding protein. rab5B.
AAG24438.1	AF304518	Oryza sativa small GTP-binding protein RAB5B. rab5B.
CAB57221.1	AJ249867	Cichorium intybus x Cichorium endivia GTP binding protein. b1.5.
CAA98180.1	Z73952	Lotus japonicus GTP-binding protein. RAB11D. rab11D.
CAA98181.1	Z73953	Lotus japonicus GTP-binding protein. RAB11E. rab11E.
BAA02114.1	D12546	Pisum sativum GTP-binding protein.
BAA02113.1	D12545	Pisum sativum GTP-binding protein.
BAA02116.1	D12548	Pisum sativum GTP-binding protein.

BAA02112.1	D12544	Pisum sativum GTP-binding protein.
BAA02118.1	D12550	Pisum sativum GTP-binding protein.
CAA98159.1	Z73931	Lotus japonicus GTP-binding protein. RAB1B. rab1B.
CAB65172.1	AJ245570	Lycopersicon esculentum putative role in secretion of cell wall modifying enzymes. Rab11 GTPase. Rab11a.
CAA89049.1	Z49190	Beta vulgaris GTP-binding. small G protein.
BAA02110.1	D12542	Pisum sativum GTP-binding protein.
AAB97114.1	U58853	Glycine max small GTP-binding protein. sra1.
BAA02904.1	D13758	Oryza sativa ras-related GTP binding protein. ss230.
CAA98178.1	Z73950	Lotus japonicus GTP-binding protein. RAB11B. rab11B.
CAA98177.1	Z73949	Lotus japonicus GTP-binding protein. RAB11A. rab11A.
AAK15703.1	AF327517	Oryza sativa GTP-binding protein.
AAF65510.1	AF108883	Capsicum annuum small GTP-binding protein.
BAA76422.1	AB024994	Cicer arietinum rab-type small GTP-binding protein.
CAA98160.1	Z73932	Lotus japonicus GTP-binding protein. RAB1C. rab1C.
AAA80680.1	U38466	Lycopersicon esculentum small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog LeRab1C.
AAA80678.1	U38464	Lycopersicon esculentum small GTP-binding protein. LeRab1A. ; YPT1/Rab1A homolog LeRab1A.
SEQ ID NO: 676		
AAA80499.1	U20594	Lycopersicon esculentum leucine aminopeptidase.
CAA54314.1	X77015	Solanum tuberosum leucine aminopeptidase. LAP.
CAA48038.1	X67845	Solanum tuberosum leucine aminopeptidase. LAP.
AAC49457.1	U50152	Lycopersicon esculentum peptidase. leucine aminopeptidase. lap2.

AAC49456.1 U50151 Lycopersicon esculentum  
exoprotease in the defense response. leucine aminopeptidase. lap.

AAA80498.1 U20593 Lycopersicon esculentum  
leucine aminopeptidase.

CAA68143.1 X99825 Petroselinum crispum  
cytosol aminopeptidase. leucine aminopeptidase.

BAA90521.1 AB037678 Phaseolus vulgaris  
leucine aminopeptidase.

SEQ ID NO: 678

CAC09580.1 AJ298992 Fagus sylvatica  
Abscisic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

AAA34002.1 M67449 Glycine max  
protein kinase. PK6.

AAK11734.1 AY027437 Arachis hypogaea  
serine/threonine/tyrosine kinase.

BAB16918.1 AP002863 Oryza sativa  
putative protein kinase. P0005A05.22.

CAA06334.1 AJ005077 Lycopersicon esculentum  
protein kinase. TCTR2 protein. TCTR2.

AAG31141.1 AF305911 Oryza sativa  
EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.

CAA73722.1 Y13273 Lycopersicon esculentum  
putative protein kinase.

AAD46406.1 AF096250 Lycopersicon esculentum  
ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to  
Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by  
GenBank Accession Number L08789.

AAG31142.1 AF305912 Hordeum vulgare  
EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.

AAD10056.1 AF110518 Lycopersicon esculentum  
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit  
ripening inducible CTR1-like protein kinase; TCTR1.

AAD10057.1 AF110519 Lycopersicon esculentum  
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit  
ripening inducible CTR1-like protein kinase; TCTR1v.

AAK30005.1 AY029067 Rosa hybrid cultivar  
CTR2 protein kinase.

BAB39409.1 AP002901 Oryza sativa  
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

BAA87853.1 AP000816 Oryza sativa  
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative  
NAK-like Ser/Thr protein kinase. (AF001308).

BAA06538.1 D31737 *Nicotiana tabacum*  
protein-serine/threonine kinase.

BAB21240.1 AP002953 *Oryza sativa*  
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

BAA94528.1 AP001800 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).

BAB17126.1 AP002867 *Oryza sativa*  
putative receptor kinase. P0463F06.16.

BAB39451.1 AP003338 *Oryza sativa*  
putative receptor kinase. OJ1212\_B09.24.

BAB17348.1 AP002747 *Oryza sativa*  
putative receptor kinase. P0698G03.32.

BAB17321.1 AP002747 *Oryza sativa*  
putative receptor kinase. P0698G03.1.

BAB17129.1 AP002867 *Oryza sativa*  
putative receptor kinase. P0463F06.20.

AAF68398.1 AF237568 *Oryza sativa*  
receptor-like protein kinase. RLG2.

BAB07905.1 AP002835 *Oryza sativa*  
putative S-receptor kinase. P0417G05.13.

BAA94517.1 AP001800 *Oryza sativa*  
Similar to *Zea mays* S-domain receptor-like protein kinase (AJ010166).

BAB17335.1 AP002747 *Oryza sativa*  
putative receptor kinase. P0698G03.17. contains ESTs D47575(S13157),AU032665(S13157).

BAB39441.1 AP003338 *Oryza sativa*  
putative receptor kinase. OJ1212\_B09.11.

BAB17116.1 AP002867 *Oryza sativa*  
putative receptor kinase. P0463F06.3.

AAF78044.1 AF248493 *Oryza sativa*  
receptor-like kinase. RLG18. protein kinase.

CAB51834.1 00069 *Oryza sativa*  
11332.5. contains eukaryotic protein kinase domain PF.

BAB17127.1 AP002867 *Oryza sativa*  
putative receptor kinase. P0463F06.17.

AAF78021.1 AF238477 *Oryza sativa*  
receptor-like kinase. RLG5. protein kinase.

AAD46420.1 AF100771 *Hordeum vulgare*  
receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.

AAD46917.1 AF164021 *Oryza sativa*  
receptor kinase.

BAB17345.1 AP002747 *Oryza sativa*  
putative receptor kinase. P0698G03.29.

BAB39438.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.7.
AAF78018.1	AF238474	Oryza sativa receptor-like kinase. RLG16. protein kinase.
AAC01746.1	AF044489	Oryza sativa receptor-like protein kinase. drpk1.
BAB17337.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.21. contains ESTs D47575(S13157),AU032665(S13157).
BAB17347.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.31. contains ESTs D47575(S13157),AU032665(S13157).
BAB17344.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.28. contains ESTs D47575(S13157),AU032665(S13157).
BAB39437.1	AP003338	Oryza sativa receptor-like kinase. OJ1212_B09.6.
AAF78019.1	AF238475	Oryza sativa receptor-like kinase. RLG17. protein kinase.
BAA05648.1	D26601	Nicotiana tabacum protein kinase.
BAB17332.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.13. contains ESTs D47575(S13157),AU032665(S13157).
BAB39435.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.2.

SEQ ID NO: 679

CAA78386.1	Z13996	Petunia x hybrida DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncogene proteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAB43399.1	AJ006292	Antirrhinum majus Myb-related transcription factor mixta-like 1. mybml1.
CAA67600.1	X99210	Lycopersicon esculentum myb-related transcription factor. THM16.
BAA23337.1	D88617	Oryza sativa transfactor. OSMYB1. Osmyb1.
AAA82943.1	U39448	Picea mariana MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
CAA64614.1	X95296	Lycopersicon esculentum transcription factor. THM27. myb-related.
BAA93038.1	AP001552	Oryza sativa EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).

AAC04720.1 AF034134 *Gossypium hirsutum*  
putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-O.  
similar to MYB A encoded by GenBank Accession Number L04497.

CAA72186.1 Y11351 *Oryza sativa*  
myb factor. myb.

AAF22256.1 AF161711 *Pimpinella brachycarpa*  
myb-related transcription factor.

BAB39987.1 AP003020 *Oryza sativa*  
putative transcription factor (myb). P0498A12.16. contains ESTs  
AU097474(S5087),D40175(S1959).

BAB39972.1 AP003018 *Oryza sativa*  
putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs  
AU097474(S5087),D40175(S1959).

BAA23338.1 D88618 *Oryza sativa*  
transfactor. OSMYB2. Osmyb2.

BAA88222.1 AB028650 *Nicotiana tabacum*  
myb-related transcription factor LBM2. lbm2.

CAA67575.1 X99134 *Lycopersicon esculentum*  
transcription factor. THM6. myb-related.

CAA78387.1 Z13997 *Petunia x hybrida*  
DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb  
proto-oncoproteins.

CAA66952.1 X98308 *Lycopersicon esculentum*  
THM18. myb-related transcription factor.

BAA23339.1 D88619 *Oryza sativa*  
transfactor. OSMYB3. Osmyb3.

AAC49394.1 U57002 *Zea mays*  
P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the  
C-terminal.

AAB41101.1 U72762 *Nicotiana tabacum*  
transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix  
motif; contains redox-sensitive cysteine.

AAA33500.1 M73028 *Zea mays*  
myb-like transcription factor. P.

AAG36774.1 AF210616 *Zea mays*  
P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.

BAA88223.1 AB028651 *Nicotiana tabacum*  
myb-related transcription factor LBM3. lbm3.

BAA88224.1 AB028652 *Nicotiana tabacum*  
myb-related transcription factor LBM4. lbm4.

CAA72187.1 Y11352 *Oryza sativa*  
myb factor. myb.

BAA88221.1 AB028649 *Nicotiana tabacum*  
myb-related transcription factor LBM1. lbm1.

CAA72185.1 Y11350 *Oryza sativa*  
myb factor. myb.

AAG13574.1 AC037425 *Oryza sativa*  
myb factor. OSJNBa0055P24.4.

SEQ ID NO: 680

AAA34238.1 L20507 *Vigna radiata*  
calmodulin.

AAA34014.1 L01432 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-3. putative.

AAA34013.1 L01430 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-1. putative.

CAA36644.1 X52398 *Medicago sativa*  
calmodulin (AA 1-149).

AAD10245.1 AF030033 *Phaseolus vulgaris*  
calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.

AAD10244.1 AF030032 *Phaseolus vulgaris*  
calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.

CAA74307.1 Y13974 *Zea mays*  
calmodulin.

CAA46150.1 X65016 *Oryza sativa*  
calmodulin. cam.

AAC36058.1 AF042839 *Oryza sativa*  
calmodulin. CaM2.

AAD10246.1 AF030034 *Phaseolus vulgaris*  
calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.

CAA54583.1 X77397 *Zea mays*  
calmodulin. CaM2.

BAA87825.1 AP000815 *Oryza sativa*  
ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene.  
Similar to *O.sativa* gene encoding calmodulin. (Z12828).

AAA92681.1 U13882 *Pisum sativum*  
calcium-binding protein. calmodulin.

AAA33706.1 M80836 *Petunia x hybrida*  
calmodulin. CAM81.

AAA33705.1 M80831 *Petunia x hybrida*  
calmodulin-related protein. CAM53.

CAA43143.1 X60738 *Malus x domestica*  
Calmodulin. CaM.

CAA78301.1 Z12839 *Lilium longiflorum*  
calcium binding protein, signal transduction. calmodulin.

AAA33397.1 L18912 *Lilium longiflorum*  
calcium binding protein, signal transduction. calmodulin. putative.

CAA42423.1 X59751 *Daucus carota*  
calmodulin. Ccam-1.

CAA67054.1 X98404 *Capsicum annuum*  
calmodulin-2.

AAG27432.1 AF295637 *Elaeis guineensis*  
calmodulin.

AAG11418.1 AF292108 *Prunus avium*  
calmodulin.

AAA34237.1 L20691 *Vigna radiata*  
calmodulin.

AAC49587.1 U49105 *Triticum aestivum*  
calmodulin TaCaM4-1. calcium-binding protein.

AAC49586.1 U49104 *Triticum aestivum*  
calmodulin TaCaM3-3. calcium-binding protein.

AAC49585.1 U49103 *Triticum aestivum*  
calmodulin TaCaM3-2. calcium-binding protein.

AAC49584.1 U48693 *Triticum aestivum*  
calmodulin TaCaM3-1. calcium-binding protein.

AAC49583.1 U48692 *Triticum aestivum*  
calmodulin TaCaM2-3. calcium-binding protein.

AAC49582.1 U48691 *Triticum aestivum*  
calmodulin TaCaM2-2. calcium-binding protein.

AAC49580.1 U48689 *Triticum aestivum*  
calmodulin TaCaM1-3. calcium-binding protein.

AAC49579.1 U48688 *Triticum aestivum*  
calmodulin TaCaM1-2. calcium binding protein.

AAC49578.1 U48242 *Triticum aestivum*  
calmodulin TaCaM1-1. calcium-binding.

AAA03580.1 L01431 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-2. putative.

AAB36130.1 S81594 *Vigna radiata*  
auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.

AAA33901.1 L18913 *Oryza sativa*  
calcium binding protein, signal transduction. calmodulin. putative.

CAA78287.1 Z12827 *Oryza sativa*  
calcium binding protein, signal transduction. calmodulin.

AAB46588.1 U83402 *Capsicum annuum*  
calmodulin.

CAA61980.1	X89890	Bidens pilosa Calmodulin.
AAA32938.1	M27303	Hordeum vulgare calmodulin.
BAA88540.1	AP000969	Oryza sativa ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAF65511.1	AF108889	Capsicum annuum calmodulin.
AAC36059.1	AF042840	Oryza sativa calmodulin. CaM1.
AAA33900.1	L18914	Oryza sativa calcium binding protein, signal transduction. calmodulin.
CAA78288.1	Z12828	Oryza sativa calcium binding protein, signal transduction. calmodulin.
AAA34015.1	L01433	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-4. putative.
AAA16320.1	L14071	Bryonia dioica calmodulin. Bc329. calcium-binding sites (amino acid #): 1. (21..33); 2. (57..68); 3. (94..106); 4. (130..141).
AAA19571.1	U10150	Brassica napus calcium binding. calmodulin. bcm1.
AAA87347.1	M88307	Brassica juncea calmodulin.
CAA52602.1	X74490	Zea mays Calmodulin. ZMCALM1.

SEQ ID NO: 683

CAA71800.1	Y10847	Brassica juncea O-acetylserine(thiol) lyase.
CAA71798.1	Y10845	Brassica juncea O-acetylserine(thiol) lyase.
AAC25635.1	AF044172	Solanum tuberosum cysteine synthase. CS-A; O-acetylserine (thiol) lyase; cytosolic isoform.
BAA01279.1	D10476	Spinacia oleracea O-acetylserine(thiol) lyase.
BAA02438.1	D13153	Triticum aestivum O-acetylserine (thiol) lyase. cys1.
CAA59798.1	X85803	Zea mays O-acetylserine (thiol) lyase. Mcysp. cysteine synthase.
AAD23907.1	AF073695	Oryza sativa cysteine synthase. rcs1. O-acetylserine(thiol)-lyase.
AAD23909.1	AF073697	Oryza sativa cysteine synthase. rcs3. O-acetylserine(thiol)-lyase.

AAC25636.1	AF044173	Solanum tuberosum cysteine synthase. CS-B; O-acetylserine (thiol) lyase; plastidic isoform.
AAC27794.1	AF078693	Chlamydomonas reinhardtii cysteine biosynthesis. putative O-acetylserine(thiol)lyase precursor. Crcys-1A.
CAA06819.1	AJ006024	Cicer arietinum cysteine synthase, O-acetyl-L-serine (thiol)-lyase.
CAA46086.1	X64874	Capsicum annuum O-acetylserine (thiol)-lyase.
CAA71799.1	Y10846	Brassica juncea O-acetylserine(thiol) lyase.
AAA16973.1	L05184	Chloroplast Spinacia oleracea O-acetylserine-(thiol)-lyase.
AAD23908.1	AF073696	Oryza sativa cysteine synthase. rcs2. O-acetylserine(thiol)-lyase.
AAD23910.1	AF073698	Oryza sativa cysteine synthase. rcs4. O-acetylserine(thiol)-lyase.
		SEQ ID NO: 684
AAA68983.1	L12395	Brassica napus signal transduction, membrane vehicle traffic. small GTP-binding protein. bra. putative.
		SEQ ID NO: 685
AAB61961.1	L81152	Oryza sativa integral membrane protein. OsNramp2.
AAB36424.1	S81897	Oryza sativa OsNramp1. OsNramp1. Nramp1 homolog/Bcg product homolog; This sequence comes from Fig. 2.
AAB62273.1	L41217	Oryza sativa integral membrane protein. OsNramp1. putative.
AAC49720.1	U60767	Oryza sativa integral membrane protein OsNramp3. OsNramp3.
		SEQ ID NO: 686
AAC04719.1	AF034133	Gossypium hirsutum putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-N. similar to MYB A encoded by GenBank Accession Number L04497.
AAB58314.1	U33917	Craterostigma plantagineum Cpm7. cpm7. putative DNA-binding protein; myb-like gene; myb-related transcription factor.
AAB58313.1	U33916	Craterostigma plantagineum Cpm5. cpm5. putative DNA-binding protein; myb-related gene; myb-related transcription factor.
AAC13876.1	U33915	Craterostigma plantagineum myb-related transcription factor Cpm10. cpm10. putative DNA-binding protein.

AAK08983.1 AY026332 *Oryza sativa*  
Myb transcription factor JAMyb. related to host cell death and defense responses; induced by jasmonic acid, wounding, or infection of rice blast fungus, but not by salicylic acid or abscisic acid.

BAB18296.1 AP002860 *Oryza sativa*  
putative myb-related transcription factor. P0409B08.23.

CAA71992.1 Y11105 *Pisum sativum*  
Myb26.

BAB40790.1 AB058642 *Lilium* hybrid division I  
LhMyb.

AAK19618.1 AF336285 *Gossypium hirsutum*  
GHMYB38. ghmyb38. similar to myb.

CAA78387.1 Z13997 *Petunia x hybrida*  
DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.

BAA88221.1 AB028649 *Nicotiana tabacum*  
myb-related transcription factor LBM1. lbm1.

BAA88224.1 AB028652 *Nicotiana tabacum*  
myb-related transcription factor LBM4. lbm4.

AAK19617.1 AF336284 *Gossypium hirsutum*  
GHMYB36. ghmyb36. similar to myb.

AAA33067.1 L04497 *Gossypium hirsutum*  
MYB A; putative.

AAK19615.1 AF336282 *Gossypium hirsutum*  
GHMYB10. ghmyb10. similar to myb.

BAA81733.2 AB029162 *Glycine max*  
GmMYB29A2.

BAA81732.1 AB029161 *Glycine max*  
GmMYB29A2.

BAA81730.1 AB029159 *Glycine max*  
GmMYB29A1.

BAA88223.1 AB028651 *Nicotiana tabacum*  
myb-related transcription factor LBM3. lbm3.

AAB41101.1 U72762 *Nicotiana tabacum*  
transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.

BAA81736.1 AB029165 *Glycine max*  
GmMYB29B2.

BAA81731.1 AB029160 *Glycine max*  
GmMYB29A1.

CAA72218.1 Y11415 *Oryza sativa*  
myb.

CAA67000.1 X98355 *Oryza sativa*  
activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like;  
expression is regulated by gibberellin.

AAK19611.1 AF336278 *Gossypium hirsutum*  
BNLGH1233. bnlghi6233. similar to myb.

CAA67575.1 X99134 *Lycopersicon esculentum*  
transcription factor. THM6. myb-related.

CAA64614.1 X95296 *Lycopersicon esculentum*  
transcription factor. THM27. myb-related.

AAD31395.1 AF114162 *Lolium temulentum*  
gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.

BAA93038.1 AP001552 *Oryza sativa*  
EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to  
*Arabidopsis thaliana* putative transcription factor (AF062916).

AAG22863.1 AY008692 *Hordeum vulgare*  
transcription factor GAMyb. Gamyb.

BAA96421.1 AB044084 *Triticum aestivum*  
transcription activator for gibberellin response. GAMyb protein. Ta-GAMyb.

CAA61021.1 X87690 *Hordeum vulgare*  
transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.

CAA66952.1 X98308 *Lycopersicon esculentum*  
THM18. myb-related transcription factor.

AAC49394.1 U57002 *Zea mays*  
P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the  
C-terminal.

BAA88222.1 AB028650 *Nicotiana tabacum*  
myb-related transcription factor LBM2. lbm2.

AAG36774.1 AF210616 *Zea mays*  
P2 protein. P2. myb-like transcriptional factor; similar to *Zea mays* P gene.

AAA33500.1 M73028 *Zea mays*  
myb-like transcription factor. P.

CAC19439.1 AJ237661 *Oryza sativa*  
Myb factor protein. myb.

CAB40189.1 AJ133638 *Avena sativa*  
transcriptional activator. myb protein. gamyb.

AAK19619.1 AF336286 *Gossypium hirsutum*  
GHMYB9. ghmyb9. similar to myb.

AAC04720.1 AF034134 *Gossypium hirsutum*  
putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-O.  
similar to MYB A encoded by GenBank Accession Number L04497.

AAC04716.1 AF034130 *Gossypium hirsutum*  
putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-D.  
similar to MYB A encoded by GenBank Accession Number L04497.

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AAG28526.1	AF198499	Nicotiana tabacum anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
CAA78388.1	Z13998	Petunia x hybrida DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
AAA33482.1	M37153	Zea mays c1 locus myb homologue; putative.
AAK09327.1	AF320614	Zea mays activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
AAK09326.1	AF320613	Zea mays activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
SEQ ID NO: 687		
BAA92972.1	AP001551	Oryza sativa ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).
BAA83689.1	AB011968	Oryza sativa OsPK7. OsPK7. protein kinase.
BAA83688.1	AB011967	Oryza sativa OsPK4. OsPK4. protein kinase.
AAF22219.1	AF141378	Zea mays protein kinase PK4. ZmPK4.
BAA34675.1	AB011670	Triticum aestivum wpk4 protein kinase. wpk4.
CAA73068.1	Y12465	Sorghum bicolor serine/threonine kinase. SNFL2.
CAA73067.1	Y12464	Sorghum bicolor serine/threonine kinase. SNFL1.
BAA92970.1	AP001551	Oryza sativa Similar to Arabidopsis thaliana chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).
CAA74646.1	Y14274	Sorghum bicolor putative serine/threonine protein kinase. SNFL3.
AAD31900.1	AF145482	Mesembryanthemum crystallinum putative serine/threonine protein kinase.
AAB62693.1	AF004947	Oryza sativa protein kinase.
BAA96628.1	AP002482	Oryza sativa ESTs D41739(S4522),AU055999(S20214), AU057588(S21592 correspond to a region of the predicted gene. Similar to Sorghum bicolor serine/threonine kinase (Y12465).

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AAD23582.1 AF128443 Glycine max  
probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.

BAA05649.1 D26602 Nicotiana tabacum  
protein kinase.

CAA71142.1 Y10036 Cucumis sativus  
SNF1-related protein kinase.

AAC99329.1 AF062479 Oryza sativa  
protein kinase SNF1. Snf1. similar to yeast SNF1.

CAA65244.1 X95997 Solanum tuberosum  
SNF1-related protein kinase. PKIN1.

CAA57898.1 X82548 Hordeum vulgare  
SNF1-related protein kinase. BKIN2.

CAA07813.1 AJ007990 Hordeum vulgare  
SnRK1-type protein kinase. kin12a.

CAA46556.1 X65606 Hordeum vulgare  
protein kinase. BKIN12.

AAB05457.1 U55768 Oryza sativa  
SNF1-related protein kinase. RSk1. Ser/Thr protein kinase homolog.

CAA46554.1 X65604 Hordeum vulgare  
protein kinase. BKIN12.

AAD00239.1 U73938 Nicotiana tabacum  
protein kinase. PK11-C1. PK11-C1. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.

AAC69450.1 AF032465 Nicotiana tabacum  
putative serine/threonine protein kinase. WAPK.

AAD00240.1 U73939 Nicotiana tabacum  
protein kinase. PK11-C5. PK11-C5. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.

BAA13608.1 D88399 Oryza sativa  
serine-threonine kinase. endosperm kinase. REK.

AAA34017.1 L19360 Glycine max  
protein kinase 2. SPK-2. putative.

AAG60195.1 AC084763 Oryza sativa  
protein kinase REK. OSJNBa0027P10.6.

AAA33004.1 L12394 Brassica napus  
serine/threonine protein kination. serine/threonine protein kinase. BSK2. putative.

BAA19573.1 AB002109 Oryza sativa  
protein kinase. a novel protein kinase.

AAA33979.1 L01453 Glycine max  
protein phosphorylation, regulatory protein. protein kinase. SPK-1. putative.

AAA33003.1 L12393 Brassica napus  
protein kination. serine/threonine protein kinase. BSK1. putative.

AAB68962.1	L38855	Glycine max protein kinase. SPK-4.
AAB68961.1	L19361	Glycine max protein kinase 3. SPK-3. putative.
AAB58348.1	U29095	Triticum aestivum serine-threonine protein kinase. TaPK3.
AAF27340.1	AF186020	Vicia faba abscisic acid-activated protein kinase. AAPK.
AAA96325.1	M94726	Triticum aestivum protein kinase. abscisic acid inducible.
CAA81443.1	Z26846	Mesembryanthemum crystallinum protein kinase. MCPK9.
AAG31326.1	AF178575	Vitis vinifera putative serine/threonine kinase GDBrPK. GDBrPK. similar to SNF protein kinase.
CAA06503.1	AJ005373	Craterostigma plantagineum protein kinase. cppk1.
AAF21062.1	AF216527	Dunaliella tertiolecta calcium-dependent protein kinase. CPK1; CDPK.
CAA89202.1	Z49233	Chlamydomonas eugametos calcium-stimulated protein kinase.
SEQ ID NO: 689		
AAC49826.1	U71604	Catharanthus roseus involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.
AAB97311.1	AF008597	Catharanthus roseus desacetoxyvindoline-4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase; involved in the second to last step in vindoline biosynthesis.
AAC49827.1	U71605	Catharanthus roseus involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.
BAA37127.1	AB012203	Lactuca sativa 2-oxoglutarate-dependent dioxygenase. gibberelin 20-oxidase. Ls20ox1.
BAA95828.1	AP002069	Oryza sativa ESTs D47168(S12332),D46350(S10967) correspond to a region of the predicted gene. Similar to Prunus armeniaca ethylene-forming-enzyme-like dioxygenase. (U97530).
AAD56580.1	AF184273	Daucus carota leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate dependent dioxygenase.
AAB39995.1	U82432	Dianthus caryophyllus anthocyanidin synthase. allele: S; 2-oxoglutarate-dependent dioxygenase.
AAD56581.1	AF184274	Daucus carota leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate dependent dioxygenase.
SEQ ID NO: 691		

AAA34002.1 M67449 Glycine max  
protein kinase. PK6.

CAC09580.1 AJ298992 Fagus sylvatica  
Abscisic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

AAK11734.1 AY027437 Arachis hypogaea  
serine/threonine/tyrosine kinase.

BAB16918.1 AP002863 Oryza sativa  
putative protein kinase. P0005A05.22.

CAA06334.1 AJ005077 Lycopersicon esculentum  
protein kinase. TCTR2 protein. TCTR2.

AAD10057.1 AF110519 Lycopersicon esculentum  
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit  
ripening inducible CTR1-like protein kinase; TCTR1v.

AAD10056.1 AF110518 Lycopersicon esculentum  
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit  
ripening inducible CTR1-like protein kinase; TCTR1.

CAA73722.1 Y13273 Lycopersicon esculentum  
putative protein kinase.

AAD46406.1 AF096250 Lycopersicon esculentum  
ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to  
Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by  
GenBank Accession Number L08789.

AAG31141.1 AF305911 Oryza sativa  
EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.

AAG31142.1 AF305912 Hordeum vulgare  
EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.

AAK30005.1 AY029067 Rosa hybrid cultivar  
CTR2 protein kinase.

AAK21965.1 AY028699 Brassica napus  
receptor protein kinase PERK1.

BAB16871.1 AP002537 Oryza sativa  
putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs  
C22608(R3192),D25110(R3192).

AAF91323.1 AF244889 Glycine max  
receptor-like protein kinase 2. RLK2. GmRLK2.

AAF91324.1 AF244890 Glycine max  
receptor-like protein kinase 3. RLK3. GmRLK3.

AAK00425.1 AC069324 Oryza sativa  
Putative protein kinase. OSJNBA0071K19.11.

BAB39409.1 AP002901 Oryza sativa  
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

AAF91322.1 AF244888 Glycine max  
receptor-like protein kinase 1. RLK1..GmRLK1.

BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
AAK16409.1	AF320086	Zea mays serine threonine kinase 1. stk1. expressed in mature tassel.
BAA06538.1	D31737	Nicotiana tabacum protein-serine/threonine kinase.
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
CAB54520.1	AJ238845	Brassica napus putative role in cell cycle control. MAP3K epsilon 1 protein kinase. MAP3K <sub>ε</sub> 1.
CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA08995.1	AJ010091	Brassica napus MAP3K alpha 1 protein kinase. MAP3K alpha 1.
BAB40094.1	AP003210	Oryza sativa putative receptor protein kinase. OSJNBa0010K01.7.
CAB51834.1	00069	Oryza sativa 11332.5. contains eukaryotic protein kinase domain PF.
BAB40021.1	AP003021	Oryza sativa putative wall-associated kinase 2. P0503E05.25. contains EST C24950(S16264).
AAF43496.1	AF131222	Lophopyrum elongatum protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum protein kinase. ESI47.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
BAB40010.1	AP003021	Oryza sativa putative wall-associated kinase 2. P0503E05.12.
AAC36318.1	AF053127	Malus x domestica leucine-rich receptor-like protein kinase. LRPKm1.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
BAB18321.1	AP002865	Oryza sativa putative receptor protein kinase. P0034C11.11.

BAA92836.1 AB032473 *Brassica oleracea*

S18 S-locus receptor kinase. SRK18.

AAA33915.1 L27821 *Oryza sativa*

receptor type serine/threonine kinase. protein kinase.

BAB40081.1 AP003074 *Oryza sativa*

putative receptor protein kinase. OSJNBa0004G10.30.

AAD38286.1 AC007789 *Oryza sativa*

putative protein kinase. OSJNBa0049B20.13.

BAA92837.1 AB032474 *Brassica oleracea*

S60 S-locus receptor kinase. SRK60.

SEQ ID NO: 692

AAK16172.1 AC079887 *Oryza sativa*

putative glucosyltransferase. OSJNBa0040E01.14.

AAF17077.1 AF199453 *Sorghum bicolor*

UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.

AAF61647.1 AF190634 *Nicotiana tabacum*

UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA89009.1 AB027455 *Petunia x hybrida*

anthocyanin 5-O-glucosyltransferase. PH1.

AAF98390.1 AF287143 *Brassica napus*

catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

AAD21086.1 AF127218 *Forsythia x intermedia*

adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.

BAA93039.1 AB033758 *Citrus unshiu*

limonoid UDP-glucosyltransferase. LGTase.

BAA83484.1 AB031274 *Scutellaria baicalensis*

UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

BAA12737.1 D85186 *Gentiana triflora*

UDP-glucose:flavonoid-3-glucosyltransferase.

CAA54612.1 X77462 *Manihot esculenta*

UTP-glucose glucosyltransferase. CGT5.

BAA19155.1 AB000623 *Nicotiana tabacum*

glucosyl transferase. JIGT.

BAA89008.1 AB027454 *Petunia x hybrida*

anthocyanidin 3-O-glucosyltransferase. PGT8.

BAB17060.1 AP002523 *Oryza sativa*

putative glucosyl transferase. P0013F10.6.

BAA90787.1 AB038248 *Ipomoea batatas*

UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.

AAK16178.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.5.

AAK16175.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.15.

AAB36653.1 U32644 *Nicotiana tabacum*  
immediate-early salicylate-induced glucosyltransferase. IS5a.

AAB36652.1 U32643 *Nicotiana tabacum*  
immediate-early salicylate-induced glucosyltransferase. IS10a.

AAK28303.1 AF346431 *Nicotiana tabacum*  
phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.

AAK28304.1 AF346432 *Nicotiana tabacum*  
phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.

BAB17061.1 AP002523 *Oryza sativa*  
putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).

CAA30761.1 X07940 *Zea mays*  
UDPGlucose flavonoid glycosyl-transferase. Bz-McC.

AAK16410.1 AF320086 *Zea mays*  
UDPG-flavonoid 3-O-glucosyl transferase. bz.

CAA31855.1 X13500 *Zea mays*  
UDPglucose:flavonol 3-0-glucosyltransferase.

BAB17059.1 AP002523 *Oryza sativa*  
putative glucosyl transferase. P0013F10.5.

BAA36421.1 AB013596 *Perilla frutescens*  
UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.

AAB86473.1 AF028237 *Ipomoea purpurea*  
UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.

CAA30760.1 X07937 *Zea mays*  
UDPglucose flavonoid glycosyl transferase. Bz-W22.

BAB41021.1 AB047094 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.

BAB41019.1 AB047092 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.

BAB41025.1 AB047098 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

AAD55985.1 AF165148 *Petunia x hybrida*  
catalyzes the penultimate step of flavonol glucosylgalactoside biosynthesis from UDP-galactose and flavonol aglycones in petunia pollen. UDP-galactose:flavonol 3-O-galactosyltransferase. F3galtase.

BAB41018.1 AB047091 *Vitis labrusca x Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents *V. vinifera* cv. Centennial.

BAB41017.1 AB047090 *Vitis labrusca x Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents *V. labruscana* cv. *Ishiharawase*.

AAK16181.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBA0040E01.16.

BAB41023.1 AB047096 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT1.

CAA59450.1 X85138 *Lycopersicon esculentum*  
tw1. homologous to glucosyltransferases.

CAA54614.1 X77464 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT7.

AAB81682.1 AF000371 *Vitis vinifera*  
UDP glucose:flavonoid 3-o-glucosyltransferase.

AAB81683.1 AF000372 *Vitis vinifera*  
UDP glucose:flavonoid 3-o-glucosyltransferase.

BAB41024.1 AB047097 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT2.

CAA54558.1 X77369 *Solanum melongena*  
glycosyl transferase. GT.

BAB41026.1 AB047099 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. FlUFGT2.

BAB41020.1 AB047093 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

BAB41022.1 AB047095 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

BAA19659.1 AB002818 *Perilla frutescens*  
flavonoid 3-O-glucosyltransferase. UDP glucose.

AAG25643.1 AF303396 *Phaseolus vulgaris*  
UDP-glucosyltransferase HRA25. putative; defense associated.

SEQ ID NO: 694

BAB40923.1 AB059401 *Oryza sativa*  
putative selenium binding protein. Os SBP.

SEQ ID NO: 695

AAD26942.1 AF119050 *Datisca glomerata*  
zinc-finger protein 1. zfp1. DgZFP1.

BAA05079.1 D26086 *Petunia x hybrida*  
zinc-finger protein.

AAB39638.1 U68763 *Glycine max*  
putative transcription factor. SCOF-1. scof-1. zinc-finger protein.

CAB77055.1 Y18788 *Medicago sativa*  
putative TFIIIA (or kruppel)-like zinc finger protein.

AAC06243.1 AF053077 *Nicotiana tabacum*  
transcription factor. osmotic stress-induced zinc-finger protein. zfp.

BAA05077.1 D26084 Petunia x hybrida  
zinc-finger DNA binding protein.

BAA05076.1 D26083 Petunia x hybrida  
zinc-finger DNA binding protein.

AAB53260.1 U76554 Brassica rapa  
transcription factor. zinc-finger protein-1. BR42.

BAA05078.1 D26085 Petunia x hybrida  
zinc-finger DNA binding protein.

AAB53261.1 U76555 Brassica rapa  
zinc-finger protein BcZFP1. BcZFP1(3-2z).

AAK01713.1 AF332876 Oryza sativa  
zinc finger transcription factor ZF1.

BAA21920.1 AB006598 Petunia x hybrida  
ZPT2-11. C2H2 zinc finger protein, 2finger.

BAA21922.1 AB006600 Petunia x hybrida  
ZPT2-13. C2H2 zinc finger protein, 2finger.

BAA19112.1 AB000453 Petunia x hybrida  
PEThy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.

BAA21927.1 AB006605 Petunia x hybrida  
ZPT3-3. C2H2 zinc finger protein, 3 finger.

BAA96071.1 AB035133 Petunia x hybrida  
C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

BAA96070.1 AB035132 Petunia x hybrida  
C2H2 zinc-finger protein ZPT2-10. PEThy;ZPT2-10.

BAA21919.1 AB006597 Petunia x hybrida  
ZPT2-10. C2H2 zinc finger protein, 2 finger.

BAA19114.1 AB000455 Petunia x hybrida  
PEThy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.

BAA21921.1 AB006599 Petunia x hybrida  
ZPT2-12. C2H2 zinc finger protein, 2 finger.

BAA21928.1 AB006606 Petunia x hybrida  
ZPT4-4. C2H2 zinc finger protein, 4 finger.

CAA60828.1 X87374 Pisum sativum  
putative zinc finger protein.

BAA21925.1 AB006603 Petunia x hybrida  
ZPT2-8. C2H2 zinc finger protein, 2 finger.

BAA19111.1 AB000452 Petunia x hybrida  
PEThy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA19926.1 AB000456 Petunia x hybrida  
PEThy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

BAA21924.1 AB006602 Petunia x hybrida  
ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA21923.1 AB006601 Petunia x hybrida  
ZPT2-14. C2H2 zinc finger protein, 2 finger.

BAA21926.1 AB006604 Petunia x hybrida  
ZPT2-9. C2H2 zinc finger protein, 2 finger.

BAA19110.1 AB000451 Petunia x hybrida  
PEThy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA19113.1 AB000454 Petunia x hybrida  
PEThy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.

SEQ ID NO: 702

AAK29419.1 AF348319 Zea mays

TERMINAL EAR1. te1. RNA-binding protein; 3 putative RRM motifs; similar to Schizosaccharomyces pombe Mei2 and Arabidopsis AML1; te1 cDNA sequence is presented in GenBank Accession Number AF047852.

CAA57551.1 X82030 Phaseolus vulgaris  
chloroplast RNA binding protein. RNP1.

CAA66479.1 X97905 Vicia faba  
RNA- or ssDNA-binding protein.

CAC01237.1 AJ292767 Nicotiana plumbaginifolia  
nuclear RNA binding protein. RNA Binding Protein 45. rbp45.

AAF66823.1 AF190655 Nicotiana tabacum  
poly(A)-binding protein. PABP.

AAK30205.1 AF349964 Daucus carota  
poly(A)-binding protein. Translin1P.

AAG59664.1 AC084319 Oryza sativa  
putative RNA binding protein. OSJNBA0004B24.1.

AAB38974.1 U81318 Triticum aestivum  
poly(A)-binding protein. wheatpab.

CAA81127.1 Z26042 Anemia phyllitidis  
Binding to the poly(A)-tail of eukaryotic mRNAs. poly(A)-mRNA binding protein.

AAA79045.1 U34742 Spinacia oleracea  
24 kDa RNA binding protein.

AAC39368.1 AF043297 Chlamydomonas reinhardtii  
poly(A) binding protein RB47. PABP.

AAF63202.1 AF240679 Cucumis sativus  
poly(A)-binding protein.

CAA11894.1 AJ224325 Hordeum vulgare  
nucleic acid-binding protein. cp33Hv.

AAF66825.1 AF190657 Nicotiana tabacum  
poly(A)-binding protein. PABP.

CAA06469.1 AJ005286 Hordeum vulgare  
nucleic acid-binding protein. cp31AHv protein.

SEQ ID NO: 709

AAB36546.1 U77940 *Phaseolus vulgaris*  
polyubiquitin. expression is regulated by heavy metal stress, UV, virus infection, heat shock  
and wounding treatment, this suggests that ubiquitin plays a role in plant defense.

SEQ ID NO: 714

CAA61946.1 X89828 *Pisum sativum*  
fructose-1,6-bisphosphate aldolase.

AAB61592.1 AF003124 *Mesembryanthemum crystallinum*  
fructose-biphosphate aldolase.

CAB77243.2 AJ133146 *Persea americana*  
glycolytic enzyme, sixth step in glycolysis. fructose-bisphosphate aldolase. alf.

BAA08845.1 D50307 *Oryza sativa*  
aldolase C-1.

BAA08830.1 D50301 *Oryza sativa*  
aldolase C-1.

CAA46649.1 X65742 *Spinacia oleracea*  
fructose-bisphosphate aldolase.

BAA02729.1 D13512 *Oryza sativa*  
cytoplasmic aldolase.

AAG21429.1 AF308587 *Fragaria x ananassa*  
cytosolic aldolase. SCA1.

CAA37290.1 X53130 *Oryza sativa*  
fructose-diphosphate aldolase (AA 1-358).

CAA31366.1 X12872 *Zea mays*  
fructose bisphosphate aldolase.

AAA33435.1 M16220 *Zea mays*  
aldolase.

CAA61947.1 X89829 *Pisum sativum*  
fructose-1,6-bisphosphate aldolase.

CAA06308.1 AJ005041 *Cicer arietinum*  
cytosolic fructose-1,6-bisphosphate aldolase.

AAK19324.1 AF329673 *Dunaliella salina*  
fructose-bisphosphate aldolase isoenzyme 1. salt-induced.

CAA71408.1 Y10380 *Solanum tuberosum*  
homologous to plastidic aldolases.

BAA77603.1 AB027002 *Nicotiana paniculata*  
plastidic aldolase.

BAA77604.1 AB027001 *Nicotiana paniculata*  
plastidic aldolase NPALDP1. NpAldP1.

AAA33642.1 M97476 *Pisum sativum*  
aldolase.

AAA33643.1 M97477 *Pisum sativum*  
aldolase.

BAA02730.1	D13513	Oryza sativa chloroplastic aldolase.
AAF74220.1	AF216582	Avena sativa fructose 1,6-bisphosphate aldolase precursor.
CAA47293.1	X66814	Spinacia oleracea fructose-bisphosphate aldolase.
AAK19325.1	AF329674	Dunaliella salina fructose-bisphosphate aldolase isoenzyme 2. salt-induced.
CAB46520.1	AJ243524	Phleum pratense sixth step in glycolysis. putative fructose-bisphosphate aldolase.
CAA09669.1	AJ011516	Scherffelia dubia fructose-bisphosphate aldolase.
CAA49590.1	X69969	Chlamydomonas reinhardtii fructose-bisphosphate aldolase. ALDCHL.
AAC60574.1	S72951	Chloroplast Chlamydomonas reinhardtii fructosediphosphate aldolase. fructosediphosphate aldolase. This sequence comes from Fig. 4.
AAB70542.1	AF017362	Oryza sativa aldolase.
BAA76430.1	AB025002	Cicer arietinum fructose-bisphosphate aldolase.
AAD20818.1	AF107590	Dendrobium grex Madame Thong-In putative fructose-bisphosphate aldolase. otg11.
BAA11395.1	D78500	Brassica rapa putative aldolase. Sequence homologous to cytoplasmic aldolase of rice (D13512).
BAA78593.1	AU066535	Chlamydomonas sp. HS-5 fructose-bisphosphate aldolase precursor. NaCl inducible.
CAC34412.1	Y18576	Flaveria trinervia fructose-bisphosphate aldolase. alf.
SEQ ID NO: 715		
AAK07429.1	AF321287	Musa acuminata beta-glucosidase.
AAC69619.1	AF072736	Pinus contorta beta-glucosidase.
AAF04007.1	AF163097	Dalbergia cochinchinensis beta-fucosidase beta-glucosidase. dalcochinin 8'-O-beta-glucoside beta-glucosidase precursor. BGLU1. rotenoid beta-glucosidase.
AAA93032.1	U50201	Prunus serotina hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase precursor. located in protein bodies of Prunus seeds; encodes 8 putative N-glycosylation sites (N-X-S/T); encodes NEP and ITENG motifs characteristic of the BGA family of beta-glucosidases.
BAA78708.1	AB003089	Polygonum tinctorium beta-glucosidase.

AAA91166.1	U39228	Prunus avium beta-glucosidase.
BAA11831.1	D83177	Costus speciosus saponin metabolite. furostanol glycoside 26-O-beta-glucosidase (F26G). functional expression in <i>E. coli</i> ; one of the F26G isozymes.
AAF34650.1	AF221526	Prunus serotina hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase isoform PHA precursor. beta-glucosidase; contains 6 potential N-glycosylation sites (N-X-S/T); glycosyl hydrolase family 1 member.
AAG25897.1	AF170087	Cucurbita pepo silverleaf whitefly-induced protein 3. SLW3. similar to beta-glucosidase.
AAG00614.1	AF293849	Secale cereale beta-glucosidase.
AAB22162.1	S35175	Manihot esculenta linamarase. linamarase. beta-glucosidase; Method: conceptual translation with partial peptide sequencing; This sequence comes from Fig. 4.
AAF03675.1	AF149311	Rauvolfia serpentina hydrolyses the glucoalkaloid raucaffricine. raucaffricine-O-beta-D-glucosidase. beta glucosidase; RG; part of the Ajmaline biosynthesis pathway; belongs to family 1 of the glucosyl hydrolases.
AAA87339.1	L41869	Hordeum vulgare beta-glucosidase. BGQ60. expression specific to starchy endosperm of seed.
AAC49177.1	U33817	Sorghum bicolor beta-glucosidase, catalyzes the hydrolysis of the cyanogenic beta-glucoside dhurrin. dhurrinase.
CAA64442.1	X94986	Manihot esculenta beta glucosidase. bglA.
AAD02839.1	AF082991	Avena sativa beta-D-glucosidase beta subunit precursor. P60b. avenacosidase.
AAD09850.1	U44087	Zea mays beta-D-glucosidase precursor. glu2. product subunit structure: autodimer of 58.4 kDa monomers Allele: glu2-B73.
AAD10503.1	U33816	Zea mays functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
AAB03266.1	U44773	Zea mays beta-D-glucosidase. glu1. autodimer of 58.4 kD monomers.
AAA65946.1	U25157	Zea mays functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
CAA52293.1	X74217	Zea mays beta-glucosidase. p60.1.

AAF28800.1 AF112888 *Catharanthus roseus*  
plays a role in secondary metabolism by hydrolyzing strictosidine to cathenamine during indole alkaloid biosynthesis. strictosidine beta-glucosidase. localized in the endoplasmic reticulum.

CAA40057.1 X56733 *Trifolium repens*  
beta-glucosidase. Li.

CAA40058.1 X56734 *Trifolium repens*  
beta-glucosidase. non-cyanogenic.

CAA55196.1 X78433 *Avena sativa*  
beta-D-glucosidase.

CAA79989.2 Z21977 *Brassica napus*  
beta thioglucosidase. myrosinase, thioglucoside glucohydrolase. Myr1.Bn1.

AAB71381.1 U95298 *Manihot esculenta*  
linamarase. pLIN-GEN. beta-glucosidase.

CAA57913.1 X82577 *Brassica napus*  
beta-glucosidase. bgl.

AAB38784.1 U72154 *Brassica nigra*  
beta-glucosidase. psr3.1. PSR3.1; phosphate-starvation responsive enzyme.

AAF34651.1 AF221527 *Prunus serotina*  
putative prunasin hydrolase precursor. beta-glucosidase; glycosyl hydrolase family 1 member.

AAA84906.1 U28047 *Oryza sativa*  
catalyzes the release of either giberellin or cyanogenic substances from their glucoconjugates. beta glucosidase. beta-D-glucoside glucohydrolase; dimer of 60 kDa monomers; localized in the plastid.

CAC08209.1 AJ005950 *Cicer arietinum*  
beta-glucosidase.

SEQ ID NO: 718

AAF61647.1 AF190634 *Nicotiana tabacum*  
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA89009.1 AB027455 *Petunia x hybrida*  
anthocyanin 5-O-glucosyltransferase. PH1.

BAA93039.1 AB033758 *Citrus unshiu*  
limonoid UDP-glucosyltransferase. LGTase.

BAA36423.1 AB013598 *Verbena x hybrida*  
UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

BAA36421.1 AB013596 *Perilla frutescens*  
UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.

AAF98390.1 AF287143 *Brassica napus*  
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

BAA36422.1 AB013597 *Perilla frutescens*  
UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.

BAB07962.1 AP002524 *Oryza sativa*  
putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs  
AU067881(C10481), AU067882(C10481).

AAD21086.1 AF127218 *Forsythia x intermedia*  
adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-  
glucosyltransferase. UFGT.

AAK16178.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.5.

BAA12737.1 D85186 *Gentiana triflora*  
UDP-glucose:flavonoid-3-glucosyltransferase.

AAK16181.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.16.

AAK16175.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.15.

AAK16172.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.14.

CAA59450.1 X85138 *Lycopersicon esculentum*  
twi1. homologous to glucosyltransferases.

AAF17077.1 AF199453 *Sorghum bicolor*  
UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-  
glucosyltransferase.

BAA89008.1 AB027454 *Petunia x hybrida*  
anthocyanidin 3-O-glucosyltransferase. PGT8.

AAB81683.1 AF000372 *Vitis vinifera*  
UDP glucose:flavonoid 3-o-glucosyltransferase.

BAB41017.1 AB047090 *Vitis labrusca x Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one  
of the parents V. labruscana cv. Ishiharawase.

AAB81682.1 AF000371 *Vitis vinifera*  
UDP glucose:flavonoid 3-o-glucosyltransferase.

BAB41022.1 AB047095 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

BAB41020.1 AB047093 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

BAB41021.1 AB047094 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.

BAB41019.1 AB047092 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.

BAA83484.1 AB031274 *Scutellaria baicalensis*  
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

BAB41025.1 AB047098 *Vitis vinifera*  
UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

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BAB41023.1 AB047096 *Vitis vinifera*  
 UDP-glucose:flavonoid 3-O-glucosyltransferase. A1UFGT1.

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BAA90787.1 AB038248 *Ipomoea batatas*  
 UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.

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BAA19659.1 AB002818 *Perilla frutescens*  
 flavonoid 3-O-glucosyltransferase. UDP glucose.

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BAB41018.1 AB047091 *Vitis labrusca x Vitis vinifera*  
 UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents *V. vinifera* cv. Centennial.

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AAB36652.1 U32643 *Nicotiana tabacum*  
 immediate-early salicylate-induced glucosyltransferase. IS10a.

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AAK28304.1 AF346432 *Nicotiana tabacum*  
 phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.

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BAB41024.1 AB047097 *Vitis vinifera*  
 UDP-glucose:flavonoid 3-O-glucosyltransferase. A1UFGT2.

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BAB41026.1 AB047099 *Vitis vinifera*  
 UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.

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CAA31855.1 X13500 *Zea mays*  
 UDPglucose:flavonol 3-O-glucosyltransferase.

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AAB86473.1 AF028237 *Ipomoea purpurea*  
 UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.

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CAA54614.1 X77464 *Manihot esculenta*  
 UTP-glucose glucosyltransferase. CGT7.

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SEQ ID NO: 719

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AAC24195.1 AF020425 *Nicotiana tabacum*  
 calmodulin binding protein. glutamate decarboxylase isozyme 1. NtGAD1. calcium-calmodulin-dependent enzyme.

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AAK18620.1 AF352732 *Nicotiana tabacum*  
 converts glutamate to gamma-aminobutyric acid. glutamate decarboxylase isozyme 3. GAD; GAD3; NtGAD3; calcium/calmodulin-dependent enzyme.

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AAB40608.1 U54774 *Nicotiana tabacum*  
 glutamate decarboxylase. NtGAD1. calmodulin regulated enzyme; calmodulin-binding protein.

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AAA33710.1 L16977 *Petunia x hybrida*  
 glutamate decarboxylase. gad.

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AAA33709.1 L16797 *Petunia x hybrida*  
 glutamate decarboxylase. gad.

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AAC39483.1 AF020424 *Nicotiana tabacum*  
 glutamate decarboxylase isozyme 2. NtGAD2. calcium-calmodulin-dependent enzyme.

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BAB32870.1 AB056062 *Oryza sativa*  
 glutamate decarboxylase. GAD.

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BAB32868.1 AB056060 *Oryza sativa*  
 glutamate decarboxylase. GAD.

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CAA56812.1 X80840 *Lycopersicon esculentum*  
homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon.

BAB32871.1 AB056063 *Oryza sativa*  
glutamate decarboxylase. GAD.

BAB32869.1 AB056061 *Oryza sativa*  
glutamate decarboxylase. GAD.

CAA50719.1 X71900 *Lycopersicon esculentum*  
histidine decarboxylase. hdc. pyridoxal 5'-phosphate dependant.

SEQ ID NO: 720

BAA92713.1 AP001389 *Oryza sativa*  
ESTs AU033035(S1515),D39871(S1515) correspond to a region of the predicted gene.  
Similar to *Arabidopsis thaliana* chromosome II BAC F22D22 genomic sequence; putative glucan synthase (AC006223).

AAD25952.1 AF085717 *Gossypium hirsutum*  
putative callose synthase catalytic subunit. CFL1. cotton FKS1-like protein; similar to *Saccharomyces cerevisiae* beta-1,3-glucan synthase subunit FKS1.

SEQ ID NO: 721

CAB55396.1 AL117264 *Oryza sativa*  
zwh12.1. similar to *Arabidopsis* putative UDP-galactose-4-epimerase (AC007060); Method: conceptual translation with partial peptide sequencing.

CAA06339.1 AJ005082 *Cyamopsis tetragonoloba*  
UDP-galactose 4-epimerase.

AAA86532.1 U31544 *Pisum sativum*  
catabolism of galactose to glucose in Leloir pathway, and in galactose synthesis from glucose.  
UDP-galactose-4-epimerase. galE. galactowaldenase.

CAA06338.1 AJ005081 *Cyamopsis tetragonoloba*  
UDP-galactose 4-epimerase.

BAB40967.1 AB059568 *Pisum sativum*  
biosynthesis of UDP-D-xylose. UDP-D-glucuronate carboxy-lyase. uxs1.

SEQ ID NO: 726

BAA88198.1 AP000837 *Oryza sativa*  
Similar to human dimethylaniline monooxygenase (AC002376).

BAA35120.1 AB008845 *Oryza sativa*  
NADH dependent Glutamate Synthase.

AAB41904.1 L37606 *Medicago sativa*  
NADH-dependent glutamate synthase.

BAA88195.1 AP000837 *Oryza sativa*  
Similar to human dimethylaniline monooxygenase (AC002376).

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AAB46617.1 L01660 *Medicago sativa*

the 3 cysteine residues in this region (amino acid residues 1246-1257) may serve to coordinate the [3Fe-4S] cluster that is probably found in this protein. See Knaff et al. (1991) *J. Biol. Chem.* 266:150. NADH-glutamate synthase. NADH-GOGAT; activity increases dramatically during nodule development; the 3 cysteine residues in this region may serve to coordinate the [3Fe-4S] cluster that is probably found in this protein. See Knaff et al. (1991) *J. Biol. Chem.* 266:15080-15084.

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SEQ ID NO: 728

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AAG43550.1 AF211532 *Nicotiana tabacum*

*Avr9/Cf-9* rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

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BAA96875.1 AB045121 *Oryza sativa*

RING finger 1. RRF1.

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AAK00436.1 AC060755 *Oryza sativa*

putative zinc finger protein. OSJNBa0003O19.23.

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BAA78746.1 AB023482 *Oryza sativa*

Similar to *Arabidopsis thaliana* RING-H2 finger protein RHX1a mRNA, partial cds.(AF079184).

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CAA74911.1 Y14573 *Hordeum vulgare*

ring finger protein. putative.

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AAG46117.1 AC073166 *Oryza sativa*

putative ring finger protein. OSJNBb0064P21.7.

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BAA85438.1 AP000616 *Oryza sativa*

similar to RING-H2 finger protein RHA1a (AF078683).

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BAA77204.1 AB026262 *Cicer arietinum*

ring finger protein.

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SEQ ID NO: 730

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AAA86424.1 U44386 *Lycopersicon esculentum*

heat shock protein. TFHS1. similar to protein encoded by the arg2 gene in mung bean, encoded by Genbank Accession Number D14411.

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SEQ ID NO: 731

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CAA06756.1 AJ005899 *Nicotiana tabacum*

G subunit. G subunit of Vacuolar-type H<sup>+</sup>-ATPase. vag1.

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CAA06757.1 AJ005900 *Nicotiana tabacum*

Subunit G of vacuolar-type H<sup>+</sup>-ATPase. vag2. vag2.

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AAD56039.1 AF184068 *Citrus limon*

vacuolar membrane ATPase subunit G. LVMA10. V-ATPase VMA10.

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SEQ ID NO: 737

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AAF69008.1 AF257779 *Oryza sativa*

stress-inducible protein. OsSII.

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SEQ ID NO: 739

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CAC12996.1 AJ299398 *Medicago truncatula*

putative auxin import. putative AUX1-like permease. lax2.

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AAF21982.1 AF115543 *Populus tremula x Populus tremuloides*  
AUX1-like protein. PAX1.

AAG17171.1 AF190880 *Populus tremula x Populus tremuloides*  
putative AUX1-like permease. pax5.

CAC12995.1 AJ299397 *Medicago truncatula*  
putative auxin import. putative AUX1-like permease. lax1.

CAC12997.1 AJ299399 *Medicago truncatula*  
putative auxin import. putative AUX1-like permease. lax3.

CAB65535.1 AJ011794 *Zea mays*  
AUX1 protein. aux1.

SEQ ID NO: 740

CAA65269.1 X96406 *Solanum tuberosum*  
13-lipoxygenase.

AAB65767.1 U37840 *Lycopersicon esculentum*  
lipoxygenase. loxD. wound, systemin and methyl-jasmonate induced.

BAA03102.1 D14000 *Oryza sativa*  
lipoxygenase. lox2osPil.

AAC12951.1 U56406 *Hordeum vulgare*  
methyljasmonate-inducible lipoxygenase 2.

CAB94852.1 AJ404331 *Prunus dulcis*  
hydroperoxydation of polyunsaturated fatty acids. lipoxygenase. lox.

AAG21691.1 AY008278 *Lycopersicon esculentum*  
lipoxygenase. oxido-reductase.

AAA79186.1 U36339 *Cucumis sativus*  
lipoxygenase.

AAB67858.1 U60200 *Solanum tuberosum*  
lipoxygenase. POTLX-1. expressed during early tuberization.

CAA64765.1 X95512 *Solanum tuberosum*  
lipoxygenase.

CAB83038.1 AJ271161 *Cucumis sativus*  
oxygenase. lipoxygenase-9. lox9.

CAA58859.1 X84040 *Nicotiana tabacum*  
lipoxygenase. Lox1.

AAB67865.1 U60202 *Solanum tuberosum*  
lipoxygenase. POTLX-3. expressed in ABA-treated leaves.

CAA55724.1 X79107 *Solanum tuberosum*  
lipoxygenase. Lox1:St:1.

AAB67860.1 U60201 *Solanum tuberosum*  
lipoxygenase. POTLX-2. expressed during early tuberization.

CAB65460.1 Y18548 *Solanum tuberosum*  
lipoxygenase. lox1-St-2.

AAD04258.1 AF039651 Solanum tuberosum  
5-lipoxygenase.

AAB81594.1 AF019613 Solanum tuberosum  
lipoxygenase. plox1.

AAA33986.1 J02795 Glycine max  
lipoxygenase-1.

AAB67732.1 U50075 Glycine max  
lipoxygenase L-5. vlxB.

CAA47717.1 X67304 Glycine max  
lipoxygenase.

AAB81595.1 AF019614 Solanum tuberosum  
lipoxygenase. plox2.

CAA64766.1 X95513 Solanum tuberosum  
lipoxygenase.

AAB31252.1 S73865 Solanum tuberosum  
linoleate:oxygen oxidoreductase. linoleate:oxygen oxidoreductase, lipoxygenase, LOX. This sequence comes from Fig. 1; lipoxygenase; LOX.

AAA53184.1 U09026 Lycopersicon esculentum  
lipoxygenase. loxA.

AAB65766.1 U37839 Lycopersicon esculentum  
lipoxygenase. loxC. expressed during ripening fruit.

CAA65268.1 X96405 Solanum tuberosum  
13-lipoxygenase.

AAF15296.2 AF204210 Phaseolus vulgaris  
lipoxygenase. LOX4.

CAA55319.1 X78581 Pisum sativum  
lipoxygenase. Lox1:Ps:3.

AAA03728.1 U04526 Glycine max  
lipoxygenase.

CAA34906.1 X17061 Pisum sativum  
lipoxygenase (AA 1-864).

CAA55318.1 X78580 Pisum sativum  
lipoxygenase. Lox1:Ps:2.

BAA03042.1 D13949 Glycine max  
lacking. lipoxygenase-2. lox2.

AAA33987.1 J03211 Glycine max  
lipoxygenase (EC 1.13.11.12).

AAB71759.1 U84198 Pisum sativum  
lipoxygenase. Lox1:Ps:1. expressed in root nodules.

AAB41272.1 U50081 Glycine max  
lipoxygenase-3.

CAA39604.1 X56139 Glycine max  
lipoxygenase. sc514.

AAA96817.1 U26457 Glycine max  
lipoxygenase. vlxC.

AAG42354.1 AF234983 Phaseolus vulgaris  
lipoxygenase.

AAG18376.1 AF283894 Zantedeschia aethiopica  
lipoxygenase. lox2.

AAD39093.1 AF095895 Oryza sativa  
catalyzes the addition of molecular oxygen to fatty acid. lipoxygenase. CM-LOX1.

CAC04380.1 AJ293015 Pisum sativum  
lipoxygenase. lox1:Ps:7.

CAA45088.1 X63525 Phaseolus vulgaris  
lipoxygenase. loxA.

AAB18970.2 U76687 Phaseolus vulgaris  
lipoxygenase. PvLOX2.

AAC49159.1 U36191 Glycine max  
linoleate:oxygen oxidoreductase. lipoxygenase. lox7.

AAA03726.1 U04785 Glycine max  
lipoxygenase.

CAA45086.1 X63521 Phaseolus vulgaris  
lipoxygenase.

SEQ ID NO: 741

AAG28436.1 AF195029 Glycine max  
plasma membrane Ca2+-ATPase. SCA2.

AAG28435.1 AF195028 Glycine max  
plasma membrane Ca2+-ATPase. SCA1.

CAA68234.1 X99972 Brassica oleracea  
calmodulin-stimulated calcium-ATPase.

AAD31896.1 AF145478 Mesembryanthemum crystallinum  
calcium ATPase.

BAA90510.2 AP001111 Oryza sativa  
rice EST AU030811, similar to rice Ca+2-ATPase (U82966).

AAD11618.1 AF050496 Lycopersicon esculentum  
Ca2+-ATPase. LCA1B; alternative transcript.

AAD11617.1 AF050495 Lycopersicon esculentum  
Ca2+-ATPase. LCA1A; alternative transcript.

AAA34138.1 M96324 Lycopersicon esculentum  
The calcium ATPase is a calcium ion pump. Ca2+-ATPase. LCA1.

CAA63790.1 X93592 Dunaliella bioculata  
P-type ATPase. ca1. calcium pumping; CA1.

AAF73985.1 AF096871 Zea mays  
calcium pump. calcium ATPase. cap1.

AAB58910.1	U82966	Oryza sativa Ca2+-ATPase.
AAD46188.1	AF156691	Nicotiana plumbaginifolia plasma membrane proton ATPase. pma9.
AAB17186.1	U72148	Lycopersicon esculentum plasma membrane H+-ATPase. LHA4. plasma membrane proton pumping ATPase.
CAA47275.1	X66737	Nicotiana plumbaginifolia plasma membrane H+-ATPase. pma4.
CAA54045.1	X76535	Solanum tuberosum H(+) -transporting ATPase. PHA2.
AAD46186.1	AF156679	Nicotiana plumbaginifolia plasma membrane proton ATPase. pma6.
CAA59800.1	X85805	Zea mays H(+) -transporting ATPase. MHA-2.
BAA06629.1	D31843	Oryza sativa plasma membrane H+-ATPase. OSA2.
AAB35314.2	S79323	Vicia faba plasma membrane H(+) -ATPase precursor. plasma membrane H(+) -ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
CAA59799.1	X85804	Phaseolus vulgaris H(+) -transporting ATPase. BHA-1.
AAB41898.1	U84891	Mesembryanthemum crystallinum plasma membrane proton pump. H+-transporting ATPase. PMA.
AAA34094.1	M80489	Nicotiana plumbaginifolia plasma membrane H+ ATPase. pma1.
AAB84202.2	AF029256	Kosteletzkya virginica plasma membrane proton ATPase. ATP1.
AAA34052.1	M27888	Nicotiana plumbaginifolia H+ -translocating ATPase.
AAA34173.1	M60166	Lycopersicon esculentum H+ -ATPase. LHA1.
AAA34098.1	M80490	Nicotiana plumbaginifolia plasma membrane H+ ATPase. pma3.
AAF98344.1	AF275745	Lycopersicon esculentum plasma membrane H+-ATPase. LHA2. P-type ion pump.
AAD55399.1	AF179442	Lycopersicon esculentum plasma membrane H+-ATPase isoform LHA2. LHA2.
CAC29436.1	AJ310524	Vicia faba P-type H+-ATPase. ha5. predominantly expressed in guard cells and flowers.
BAA08134.1	D45189	Zostera marina plasma membrane H+-ATPase. zha1.

BAA01058.1	D10207	Oryza sativa H-ATPase. OSA1.
CAB69824.1	AJ271439	Prunus persica plasma membrane H <sup>+</sup> ATPase. PPA1.
CAA54046.1	X76536	Solanum tuberosum H(+) -transporting ATPase. PHA1.
AAB60276.1	U09989	Zea mays H(+) -transporting ATPase. Mha1.
CAB69823.1	AJ271438	Prunus persica plasma membrane H <sup>+</sup> ATPase. PPA2.
AAK31799.1	AY029190	Lilium longiflorum plasma membrane H <sup>+</sup> ATPase. LILHA1.
BAA37150.1	AB022442	Vicia faba p-type H <sup>+</sup> -ATPase. VHA2.
CAC29435.1	AJ310523	Vicia faba P-type H <sup>+</sup> -ATPase. vha4. predominantly expressed in flowers.
CAB85495.1	AJ132892	Medicago truncatula proton pump. H <sup>+</sup> -ATPase. ha1.
CAB85494.1	AJ132891	Medicago truncatula proton pump. H <sup>+</sup> -ATPase. ha1.
AAD46187.1	AF156683	Nicotiana plumbaginifolia plasma membrane proton ATPase. pma8.
AAD29712.1	AF140499	Oryza sativa chloroplast envelope calcium ATPase precursor.
AAK32118.1	AF308816	Hordeum vulgare plasmalemma H <sup>+</sup> -ATPase 1.
AAG01028.1	AF289025	Cucumis sativus plasma membrane H <sup>+</sup> -ATPase.
AAF97591.1	AF263917	Lycopersicon esculentum plasma membrane proton ATPase. LHA8.
AAA81348.1	U38965	Vicia faba p-type H <sup>+</sup> -ATPase. VHA2.
AAA20600.1	U08984	Zea mays plasma-membrane H <sup>+</sup> ATPase. Zmpma1.
AAA20601.1	U08985	Zea mays plasma-membrane H <sup>+</sup> ATPase. Zmpma1.
AAK32119.1	AF308817	Hordeum vulgare plasmalemma H <sup>+</sup> -ATPase 2.
SEQ ID NO: 742		
AAD02548.1	AF049922	Petunia x hybrida PGPS/D6. PGPS/D6. ER lumen protein retaining receptor homolog; putative HDEL receptor.
SEQ ID NO: 744		

AAG13424.1	AC051634	Oryza sativa putative mitochondrial inner membrane protein. OSJNBb0018B10.5.
AAG46068.1	AC079830	Oryza sativa putative inner mitochondrial membrane protein. OSJNBb0009F04.14.
SEQ ID NO: 746		
BAA32557.1	AB017159	Daucus carota citrate synthase. DcCS.
AAA82743.1 U19481 Citrus maxima synthesis of citrate from oxaloacetate and acetylCoA. citrate synthase precursor. cit.		
AAG28777.1	AF302906	Oryza sativa citrate synthase. similar to putative Oryza sativa citrate synthase in GenBank Accession Number AC004521.
CAA59008.1	X84226	Nicotiana tabacum citrate synthase. cit1.
CAA52976.1	X75082	Solanum tuberosum mitochondrial citrate-synthase. ethanolamine ammonia-lyase.
BAA82390.1	AP000367	Oryza sativa ESTs C96653(C10531),C96654(C10531),C28571(C61641) correspond to a region of the predicted gene.; Similar to citrate synthetase. (AC004521).
CAA59010.1	X84228	Beta vulgaris citrate (si)-synthase. cit1.
CAA59009.1	X84227	Populus x generosa citrate (si)-synthase. cit1.
BAA07328.1	D38132	Cucurbita sp. conversion of oxaloacetate to citrate in the glyoxylate cycle. glyoxysomal citrate synthase.
SEQ ID NO: 750		
AAA85365.1	L42466	Picea glauca ethylene-forming enzyme. EFE.
AAC95363.1	AF104925	Solanum chacoense 2-oxoglutarate-dependent dioxygenase. SPP2. pollination and fertilization induced gene.
BAA75309.1	AB023790	Ipomoea batatas flavanone 3-hydroxylase. f3h III.
BAA75308.1	AB023789	Ipomoea batatas flavanone 3-hydroxylase. f3h II.
BAA75306.1	AB023787	Ipomoea batatas anthocyanidin synthase. ans II.
AAC48922.1	U06047	Vigna radiata 1-aminocyclopropane-1-carboxylate oxidase homolog.
SEQ ID NO: 751		
BAB40010.1	AP003021	Oryza sativa putative wall-associated kinase 2. P0503E05.12.
BAA95893.1	AP002071	Oryza sativa Similar to Arabidopsis thaliana wak4 gene; wall-associated kinase 4. (AJ009695).

BAB40015.1	AP003021	Oryza sativa putative wall-associated kinase 1. P0503E05.18.
BAA92221.1	AP001278	Oryza sativa Similar to <i>Arabidopsis thaliana</i> chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	Oryza sativa Similar to putative Ser/Thr protein kinase. (AC004218).
BAB40021.1	AP003021	Oryza sativa putative wall-associated kinase 2. P0503E05.25. contains EST C24950(S16264).
CAB51834.1	00069	Oryza sativa I1332.5. contains eukaryotic protein kinase domain PF.
AAB09771.1	U67422	Zea mays CRINKLY4 precursor. cr4. receptor kinase homolog.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK11566.1	AF318490	Lycopersicon hirsutum Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB40022.1	AP003021	Oryza sativa putative wall-associated kinase 1. P0503E05.26.
CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1A <i>Arabidopsis thaliana</i> . P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAK11674.1	AF339747	Lophopyrum elongatum protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
BAA90808.1	AP001168	Oryza sativa Similar to putative receptor-like protein kinase (AL035679).
AAF76313.1	AF220603	Lycopersicon esculentum Pto kinase. LescPth5.
AAB47421.1	U59316	Lycopersicon esculentum serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

AAB47423.1 U59315 *Lycopersicon pimpinellifolium*  
serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease  
resistance gene.

AAC48914.1 U02271 *Lycopersicon pimpinellifolium*  
protein kinase.

AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*  
Pto kinase.

AAG59657.1 AC084319 *Oryza sativa*  
putative protein kinase. OSJNBA0004B24.20.

AAK11567.1 AF318491 *Lycopersicon hirsutum*  
Pto-like protein kinase F. LhirPtoF.

AAK21965.1 AY028699 *Brassica napus*  
receptor protein kinase PERK1.

AAG25966.1 AF302082 *Nicotiana tabacum*  
cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly  
after cytokinin treatment.

AAK11569.1 AF318493 *Lycopersicon hirsutum*  
Pto-like protein kinase D. LhirPtoD.

AAF66615.1 AF142596 *Nicotiana tabacum*  
LRR receptor-like protein kinase.

AAG03090.1 AC073405 *Oryza sativa*  
Similar to an *Arabidopsis* somatic embryogenesis receptor-like kinase (AC007504).

BAA87853.1 AP000816 *Oryza sativa*  
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative  
NAK-like Ser/Thr protein kinase. (AF001308).

BAA83373.1 AP000391 *Oryza sativa*  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar  
to receptor protein kinase, ERECTA (AC004484).

BAA84787.1 AP000559 *Oryza sativa*  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar  
to receptor protein kinase, ERECTA (AC004484).

CAA74662.1 Y14286 *Brassica oleracea*  
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular  
kinase domain: from 1413.

CAA67145.1 X98520 *Brassica oleracea*  
receptor-like kinase. SFR2.

CAA73133.1 Y12530 *Brassica oleracea*  
serine /threonine kinase. ARLK.

AAK11568.1 AF318492 *Lycopersicon hirsutum*  
Pto-like protein kinase B. LhirPtoB.

BAA78764.1 AB023482 *Oryza sativa*  
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar  
to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAK00425.1 AC069324 *Oryza sativa*  
Putative protein kinase. OSJNBa0071K19.11.

AAK31267.1 AC079890 *Oryza sativa*  
putative protein kinase. OSJNBb0089A17.2.

BAA94509.1 AB041503 *Populus nigra*  
protein kinase 1. PnPK1.

BAA94510.1 AB041504 *Populus nigra*  
protein kinase 2. PnPK2.

SEQ ID NO: 752

BAB39155.1 AB048713 *Pisum sativum*  
SCARECROW. PsSCR.

AAG13663.1 AF263457 *Zea mays*  
transcription factor. SCARECROW. SCR. ZmSCR.

BAA90816.1 AP001168 *Oryza sativa*  
Similar to SCARECROW (U62798).

AAC98090.1 AF067400 *Zea mays*  
Scl1 protein. Scl1. Scarecrow-like; similar to Zea mays sequence presented in GenBank  
Accession Number T18310.

BAB39156.1 AB048714 *Pisum sativum*  
SCARECROW. PsSCR.

SEQ ID NO: 753

AAF21901.1 AF109392 *Brassica napus*  
ligand gated channel-like protein. glutamate receptor homolog.

SEQ ID NO: 757

CAA92821.1 Z68504 *Oryza sativa*  
3-hydroxy-3-methylglutaryl-CoA reductase.

AAA33360.1 M74800 *Hevea brasiliensis*  
3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.

CAA70440.1 Y09238 *Zea mays*  
3-hydroxy-3-methylglutaryl coenzyme A reductase.

AAB69727.1 U72146 *Camptotheca acuminata*  
3-hydroxy-3-methylglutaryl coenzyme A reductase. converts HMGC-CoA in mevalonate  
precursor for isoprenoid compounds; HMGR; hmg2; similar to protein encoded by GenBank  
Accession Number L10390.

AAD08820.1 U43961 *Oryza sativa*  
3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.

AAA68965.1 U14624 *Artemisia annua*  
3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM1.

AAD47596.1 AF142473 *Artemisia annua*  
HMG-CoA reductase. HMGR1.

AAD03789.1 U43711 *Morus alba*  
catalyzes the final step in mevalonate pathway. 3-hydroxy-3-methylglutaryl-coenzyme A  
reductase. HMGR.

AAA33108.1 M96068 *Catharanthus roseus*  
hydroxymethylglutaryl-CoA reductase. HMGR.

CAA48610.1 X68651 *Raphanus sativus*  
hydroxymethylglutaryl-CoA reductase (NADPH). HMG1.

AAA93498.1 L01400 *Solanum tuberosum*  
convert HMG-CoA into mevalonate. hydroxymethylglutaryl coenzyme A reductase. hmgr.  
putative.

AAA68966.1 U14625 *Artemisia annua*  
3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM4.

AAB52552.1 U51986 *Solanum tuberosum*  
HMG-CoA reductase.

CAA48611.1 X68652 *Raphanus sativus*  
hydroxymethylglutaryl-CoA reductase (NADPH). HMG2.

BAA93631.1 AB022690 *Solanum tuberosum*  
3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG3.

AAB62581.1 U68072 *Lycopersicon esculentum*  
3-hydroxy-3-methylglutaryl CoA reductase 2. HMG2.

AAA34169.1 M63642 *Lycopersicon esculentum*  
3-hydroxy-3-methylglutaryl coenzyme A reductase. hmg2.

AAB69726.1 U72145 *Camptotheca acuminata*  
converts HMGCoA to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme a reductase. hmg3.  
HMGR.

AAB52551.1 U51985 *Solanum tuberosum*  
HMG-CoA reductase.

AAA33040.1 L10390 *Camptotheca acuminata*  
3-hydroxy-3-methylglutaryl coA reductase.

AAD28179.1 AF110383 *Capsicum annuum*  
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR2M. HMGR.

BAB20771.1 AB041031 *Solanum tuberosum*  
3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG2.

AAB53748.1 U95816 *Oryza sativa*  
3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.

AAC05088.1 AF038045 *Gossypium hirsutum*  
catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme  
A reductase 1. hmg1. hmg-coA reductase 1; HMGR1.

CAA45181.1 X63649 *Nicotiana sylvestris*  
catalyses synthesis of mevalonate. 3-hydroxy-3-methylglutaryl-coenzyme A reductase.  
HMGR. endoplasmic reticulum location.

CAA38469.1 X54659 *Hevea brasiliensis*  
hydroxymethylglutaryl-CoA reductase. HMGR1.

CAA38467.1 X54657 *Hevea brasiliensis*  
hydroxymethylglutaryl-CoA reductase. HMGR1.

AAD38873.1	AF110382	Oryza sativa 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR3G. HMG-CoA reductase.
BAA36291.1	AB021862	Cucumis melo HMG-CoA reductase. Cm-HMGR. putative.
AAB87727.1	U60452	Nicotiana tabacum hydroxy-methylglutaryl-coenzyme A reductase. HMGR1.
AAC05089.1	AF038046	Gossypium hirsutum catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2. hmg2. hmg-coA reductase 2; HMGR2.
AAC15475.1	AF034760	Tagetes erecta 3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAC15476.1	AF034761	Tagetes erecta 3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAA21720.1	L28995	Oryza sativa conversion of hydroxymethylglutaryl coenzyme A to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme A reductase. putative.
AAA33358.1	M74798	Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
AAC72378.1	AF096838	Solanum tuberosum 3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAB04043.1	L40938	Lycopersicon esculentum HMGR CoA reductase. HMGR1.
CAA38468.1	X54658	Hevea brasiliensis hydroxymethylglutaryl-CoA reductase. HMGR2.
CAA52787.1	X74783	Lithospermum erythrorhizon 3-hydroxy-3-methyl glutaryl coenzyme A reductase. Lehmg1.
AAD09278.1	U97683	Glycine max catalyzes the synthesis of mevalonate, the specific precursor of all isoprenoid compounds present in plants. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMG-CoA reductase.
AAG43469.1	AF196964	Bixa orellana catalyzes mevalonate synthesis from hmg-CoA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase.
BAA09705.1	D63389	Cucumis sativus 3-hydroxy-3-methylglutaryl CoA reductase.
AAB47161.1	S82272	Gossypium barbadense 3-hydroxy-3-methylglutaryl coenzyme A reductase. /gene="3-hydroxy-3-methylglutaryl coenzyme A reductase,. This sequence comes from Fig. 2; 3-hydroxy-3-methylglutaryl CoA reductase; HMGR.
AAA33359.1	M74799	Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
AAC37434.1	L34827	Solanum tuberosum HMG-CoA reductase. hmg1 gene family.

AAC37432.1 L34825 Solanum tuberosum  
HMG-CoA reductase. hmg1 gene family.

AAC37435.1 L34828 Solanum tuberosum  
HMG-CoA reductase. hmg1 gene family.

AAC37433.1 L34826 Solanum tuberosum  
HMG-CoA reductase. hmg1 gene family.

AAC37431.1 L34823 Solanum tuberosum  
HMG-CoA reductase. hmg1 gene family.

SEQ ID NO: 761

CAA96512.1 Z71980 Malus x domestica  
knotted1-like homeobox protein.

BAA25921.1 AB004797 Nicotiana tabacum  
NTH23. homeobox gene.

AAD09582.1 U76409 Lycopersicon esculentum  
homeobox 1 protein. THox1. homeodomain protein.

AAC49918.1 AF000142 Lycopersicon esculentum  
class II knotted-like homeodomain protein. LeT12.

BAA08552.1 D49704 Oryza sativa  
OSH45. OSH44 transcript homeobox gene.

BAB18585.1 AB043957 Ceratopteris richardii  
CRKNOX3. crknox3. knotted1-like homeodomain protein.

AAD00253.1 U76410 Lycopersicon esculentum  
homeobox 2 protein. THox2. homeodomain protein.

CAA82314.1 Z29073 Brassica napus  
homeodomain-containing protein. Bnhd1.

BAA77822.1 AB007628 Oryza sativa  
HOS59. homeobox gene.

BAA77823.1 AB007629 Oryza sativa  
HOS66. homeobox gene.

AAB81079.1 AF022390 Hordeum vulgare  
knotted class 1 homeodomain protein. k. similar to the hooded gene product encoded by  
GenBank Accession Number X83518; similar to the maize knotted-1 gene product encoded  
by GenBank Accession Number X61308.

AAF32399.1 AF224499 Triticum aestivum  
KNOTTED-1-like homeobox protein b. knox1b. KNOX1b.

BAA76750.1 AB025573 Nicotiana tabacum  
KN1-type homeobox protein. NTH1.

AAF32400.1 AF224500 Triticum aestivum  
KNOTTED-1-like homeobox protein d. knox1d. KNOX1d.

AAC49917.1 AF000141 Lycopersicon esculentum  
class I knotted-like homeodomain protein. LeT6.

BAA25546.1 AB004785 Nicotiana tabacum  
NTH15. homeobox gene.

AAF32398.1	AF224498	Triticum aestivum KNOTTED-1-like homeobox protein a. knox1a. KNOX1.
AAD13611.1	AF100455	Zea mays knotted class 1 homeodomain protein liguleless3. lg3.
AAC84001.1	AF063248	Picea abies homeobox protein.
AAC33008.1	AF080104	Pisum sativum knotted1-like class I homeodomain protein. PsKn1.
AAD00692.1	U90092	Picea mariana homeobox transcription factor SKN2. knotted1-like homeobox gene.
AAC32262.1	AF063307	Pisum sativum Knox class 1 protein. Hop1.
BAA03959.1	D16507	Oryza sativa homeobox protein. OSH1.
AAG27464.1	AF308454	Medicago truncatula knotted class I homeodomain KNOX.
AAD00691.1	U90091	Picea mariana homeobox transcription factor SKN1. knotted1-like homeobox gene.
AAC32817.1	AF050180	Oryza sativa transcription factor. KNOX class homeodomain protein. OsKn2.
BAA79226.1	AB028885	Oryza sativa knotted1-type homeobox protein OSH71. OSH71.
BAA79224.1	AB028883	Oryza sativa knotted1-type homeobox protein OSH6. OSH6.
BAA77818.1	AB007624	Oryza sativa HOS9. homeobox gene.
BAB19772.1	AP002881	Oryza sativa putative knotted1-type homeobox protein. P0035H10.13.
AAF23753.2	AF193813	Brassica oleracea shoot meristemless. Stm. homeodomain protein.
AAD00251.1	U76407	Lycopersicon esculentum knotted 2 protein. TKn2. homeodomain protein.
CAA96510.1	Z71978	Malus x domestica kn1-like protein.
BAA31688.1	AB016071	Oryza sativa OSH15. homeobox gene.
BAA77817.1	AB007623	Oryza sativa HOS3. homeobox gene.
BAB18582.1	AB043954	Ceratopteris richardii CRKNOX1. crknox1. knotted1-like homeodomain protein.
BAA76903.1	AB025713	Nicotiana tabacum homeobox 9. NTH9.

AAD00252.1 U76408 *Lycopersicon esculentum*  
knotted 3 protein. TKn3. homeodomain protein.

BAB18584.1 AB043956 *Ceratopteris richardii*  
CRKNOX2. crknox2. knotted1-like homeodomain protein.

CAA96511.1 Z71979 *Malus x domestica*  
kn1-like protein.

AAA20882.1 L13663 *Glycine max*  
SBH1. Sbh1. soybean homeobox-containing gene.

CAB88029.1 AJ276389 *Dendrobium grex Madame Thong-In*  
transcription factor. knotted1-like homeobox protein.

SEQ ID NO: 762

AAB65776.1 U97521 *Vitis vinifera*  
class IV endochitinase. VvChi4A.

AAB65777.1 U97522 *Vitis vinifera*  
class IV endochitinase. VvChi4B.

CAA53626.1 X76041 *Triticum aestivum*  
endochitinase. CHI.

AAG53609.1 AF280437 *Secale cereale*  
31.7 kDa class I endochitinase-antifreeze protein precursor. cht9.

BAA03750.1 D16222 *Oryza sativa*  
endochitinase. Cht-2.

AAA32986.1 M95835 *Brassica napus*  
endochitinase. Ch25.

BAA03749.1 D16221 *Oryza sativa*  
endochitinase. Cht-1.

AAB01895.1 U48687 *Castanea sativa*  
endochitinase.

SEQ ID NO: 763

AAA34065.1 M94135 *Nicotiana tabacum*  
chloroplast carbonic anhydrase.

AAA34057.1 L19255 *Nicotiana tabacum*  
carbonic anhydrase.

AAB65822.1 U55838 *Populus tremula x Populus tremuloides*  
carbonic anhydrase. CA1b. EC 4.2.1.1.

AAC49785.1 U55837 *Populus tremula x Populus tremuloides*  
carbonic anhydrase. CA1a. EC 4.2.1.1.

AAA34026.1 M27295 *Spinacia oleracea*  
carbonic anhydrase precursor.

AAA34027.1 J05403 *Spinacia oleracea*  
carbonic anhydrase (EC 4.2.1.1).

AAA86993.1 U19738 *Flaveria linearis*  
reversible hydration of carbon dioxide. carbonic anhydrase 1.

AAA86942.1 U08402 *Flaveria brownii*  
carbonic anhydrase.

AAA86992.1 U19737 *Flaveria pringlei*  
reversible hydration of carbon dioxide. carbonic anhydrase.

AAA86939.1 U08398 *Flaveria bidentis*  
carbonic anhydrase.

AAD27876.2 AF139464 *Vigna radiata*  
carbonic anhydrase. CipCal.

AAA33652.1 M63627 *Pisum sativum*  
carbonic anhydrase.

AAD29050.1 AF132855 *Gossypium hirsutum*  
interconversion of CO<sub>2</sub> and HCO<sub>3</sub><sup>-</sup>. carbonic anhydrase isoform 2. CA2. zinc metalloenzyme;  
carbonate dehydratase.

AAD29049.1 AF132854 *Gossypium hirsutum*  
interconversion of CO<sub>2</sub> and HCO<sub>3</sub><sup>-</sup>. carbonic anhydrase isoform 1. CA1. zinc metalloenzyme;  
carbonate dehydratase.

AAA86994.1 U19740 *Flaveria linearis*  
reversible hydration of carbon dioxide. carbonic anhydrase 2.

CAB43571.1 AJ239132 *Glycine max*  
hydration of carbon dioxide. carbonic anhydrase. cal.

CAA63712.1 X93312 *Medicago sativa*  
Carbonic anhydrase. cal.

AAA86945.1 U08403 *Zea mays*  
carbonic anhydrase.

AAA86944.1 U08401 *Zea mays*  
carbonic anhydrase.

AAC41656.1 L36959 *Hordeum vulgare*  
carbonic anhydrase. putative.

AAA86943.1 U08404 *Oryza sativa*  
carbonic anhydrase. nuclear encoded, localized to chloroplast.

AAD56038.1 AF182806 *Oryza sativa*  
carbonic anhydrase 3. ca3.

BAA31953.1 AB016283 *Oryza sativa*  
carbonic anhydrase.

AAA69027.1 U19739 *Urochloa panicoides*  
reversible hydration of carbon dioxide. carbonic anhydrase 2.

AAA69028.1 U19741 *Urochloa panicoides*  
reversible hydration of carbon dioxide. carbonic anhydrase 1.

BAA95793.1 AB009887 *Nicotiana tabacum*  
carbonic anhydrase. carbonic anhydrase.

AAF78507.1 AF195204 *Pyrus pyrifolia*  
carbonic anhydrase isoform 1. CA1.

AAC33484.1 U49976 *Coccomyxa* sp. PA  
beta-type carbonic anhydrase beta-CA1.

AAA18560.1 M95073 *Zea mays*  
putative. silimar to carbonic anhydrases.

AAB19184.1 U41190 *Chlamydomonas reinhardtii*  
carbonic anhydrase precursor. beta-CA2.

AAB19183.1 U41189 *Chlamydomonas reinhardtii*  
carbonic anhydrase precursor. beta-CA1.

AAC49887.1 U80804 *Chlamydomonas reinhardtii*  
beta-carbonic anhydrase. ca1. beta-CA1.

AAC49888.1 U80805 *Chlamydomonas reinhardtii*  
beta-carbonic anhydrase. ca2. beta-CA2.

SEQ ID NO: 764

AAC06027.1 AF052058 *Vigna unguiculata*  
iron storage and mobilization in plants. ferritin subunit cowpea2 precursor.

AAD50644.1 AF133814 *Solanum tuberosum*  
ferritin 1. F1.

AAB53099.1 U68217 *Brassica napus*  
iron binding protein. ferritin. LSC30.

AAA33959.1 M64337 *Glycine max*  
ferritin light chain. ferritin.

AAA34016.1 M72894 *Glycine max*  
ferritin light chain. SOF-H2.

CAA58146.1 X83076 *Zea mays*  
ferritin. Fer1.

AAB18928.1 U31648 *Glycine max*  
iron storage protein. ferritin.

CAA65771.1 X97059 *Medicago sativa*  
iron storage. ferritin. FER. abscissic acid regulated.

CAA43663.1 X61391 *Zea mays*  
ferritin.

CAA58147.1 X83077 *Zea mays*  
ferritin. Fer2.

AAC06026.1 AF052057 *Vigna unguiculata*  
iron storage and mobilization in plants. ferritin subunit cowpea3 precursor.

CAA43664.1 X61392 *Zea mays*  
ferritin.

CAA51786.1 X73369 *Pisum sativum*  
ferritin.

CAA45763.1 X64417 *Pisum sativum*  
ferritin-precursor.

CAA41213.1	X58274	Phaseolus vulgaris ferritin. pfe.
AAA33958.1	M58336	Glycine max ferritin light chain. SOF-5L.
CAB42587.1	AJ238628	Chlorella protothecoides putative ferritin. dee188.
BAB17852.1	AB042612	Nicotiana tabacum ferritin 1. tob-fer-1. putative.
AAC15241.1	AF028072	Pinus taeda ferritin.
CAA47983.1	X67755	Vigna unguiculata ferritin 2. pfe2.
CAA47982.1	X67754	Vigna unguiculata ferritin 1. pfe1.
CAA47984.1	X67756	Vigna unguiculata ferritin 5. pfe5.
AAC12282.1	AF052511	Glycine max iron storage and mobilization. ferritin 2. soybean 2; cowpea 2 homolog.
AAC12281.1	AF052513	Glycine max iron storage and mobilization. ferritin 1. soybean 1; cowpea 1 homolog.
SEQ ID NO: 765		
AAC36697.1	AF075579	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAC10358.1	AJ277086	Nicotiana tabacum protein phosphatase 2C. PP2C1.
CAB90633.1	AJ277743	Fagus sylvatica protein phosphatase 2C (PP2C). pp2C1. ABA-induced protein.
AAD17804.1	AF092431	Lotus japonicus nodule-enhanced protein phosphatase type 2C. NPP2C1.
CAC10359.1	AJ277087	Nicotiana tabacum protein phosphatase 2C. PP2C2.
CAC09575.1	AJ298987	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf1.
CAA72341.1	Y11607	Medicago sativa protein phosphatase 2C. MP2C.
CAB61839.1	AJ242803	Sporobolus stapfianus putative serine/threonine phosphatase type 2c.
AAD17805.1	AF092432	Lotus japonicus protein phosphatase type 2C. PP2C2.
AAG43835.1	AF213455	Zea mays protein phosphatase type-2C. pp2c-1. PP2C-1.

AAG46118.1	AC073166	Oryza sativa putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
AAG13599.1	AC051633	Oryza sativa putative protein phosphatase-2C. OSJNBb0015I11.26.
AAC36698.1	AF075580	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
BAB12036.1	AP002820	Oryza sativa putative protein phosphatase. P0702D12.18.
AAC36700.1	AF075582	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
AAC36699.1	AF075581	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
AAK20060.1	AC025783	Oryza sativa putative protein phosphatase 2C. OSJNBa0001O14.1.
AAD11430.1	AF097667	Mesembryanthemum crystallinum protein phosphatase 2C homolog. PP2C.
CAB90634.1	AJ277744	Fagus sylvatica protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
AAC35951.1	AF079355	Mesembryanthemum crystallinum protein phosphatase-2c. PP2C.
AAF19804.1	AF180355	Brassica oleracea ABI1 protein. ABI1. similar to Arabidopsis thaliana ABI1.
AAB93832.1	U81960	Zea mays kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
AAC26828.1	AF075603	Oryza sativa kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
CAC09576.1	AJ298988	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf2.
SEQ ID NO: 766		
AAG08959.1	AF122051	Solanum tuberosum tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08960.1	AF122052	Solanum tuberosum tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08961.1	AF122053	Solanum tuberosum tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.

BAA88169.1 AP000836 Oryza sativa  
Similar to putative transcription factor (AF062890).

BAA88205.1 AP000837 Oryza sativa  
Similar to putative transcription factor (AF062890).

AAF34434.1 AF172282 Oryza sativa  
myb-like protein. DUPR11.29.

AAF78890.1 AF189788 Hordeum vulgare  
putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.

AAF78889.1 AF189787 Hordeum vulgare  
putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.

AAF67053.1 AF190304 Adiantum raddianum  
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.

AAF67052.1 AF190303 Adiantum raddianum  
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.

AAF78888.1 AF189786 Physcomitrella patens  
putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.

AAF78887.1 AF189785 Physcomitrella patens  
putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.

AAF43043.1 AF236059 Papaver rhoes  
putative Myb-related domain. pmr.

BAA94769.1 AP001859 Oryza sativa  
Similar to Arabidopsis thaliana chromosome 4, BAC clone F4D11; putative myb-protein. (AL022537).

AAF67050.1 AF190301 Secale cereale  
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.

AAF67051.1 AF190302 Secale cereale  
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.

CAA78388.1 Z13998 Petunia x hybrida  
DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.

BAB39987.1 AP003020 Oryza sativa  
putative transcription factor (myb). P0498A12.16. contains ESTs  
AU097474(S5087),D40175(S1959).

BAB39972.1 AP003018 Oryza sativa  
putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs  
AU097474(S5087),D40175(S1959).

CAA72218.1 Y11415 Oryza sativa  
myb.

BAA81731.1 AB029160 Glycine max  
GmMYB29A1.

BAA81730.1 AB029159 Glycine max  
GmMYB29A1.

CAA72217.1 Y11414 Oryza sativa  
myb.

BAA81736.1 AB029165 Glycine max  
GmMYB29B2.

BAB12688.1 AP002746 Oryza sativa  
putative MYB family transcription factor. P0671B11.3. contains ESTs  
AU082307(E0784),C72014(E0784).

BAA99440.1 AP002743 Oryza sativa  
putative MYB family transcription factor. P0710E05.27. contains ESTs  
AU082307(E0784),C72014(E0784).

AAB41101.1 U72762 Nicotiana tabacum  
transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix  
motif; contains redox-sensitive cysteine.

BAA88223.1 AB028651 Nicotiana tabacum  
myb-related transcription factor LBM3. lbm3.

BAA23340.1 D88620 Oryza sativa  
transfactor. OSMYB4. Osmyb4.

BAA93038.1 AP001552 Oryza sativa  
EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to  
Arabidopsis thaliana putative transcription factor (AF062916).

AAA33067.1 L04497 Gossypium hirsutum  
MYB A; putative.

BAA81733.2 AB029162 Glycine max  
GmMYB29A2.

BAA88222.1 AB028650 Nicotiana tabacum  
myb-related transcription factor LBM2. lbm2.

CAB43399.1 AJ006292 Antirrhinum majus  
Myb-related transcription factor mixta-like 1. mybml1.

BAA81732.1 AB029161 Glycine max  
GmMYB29A2.

AAG28525.1 AF198498 Nicotiana tabacum  
anther-specific myb-related protein 2. mybAS2. NtMYBAS2; contains tandem R2, R3 myb  
domains similar to c-myb family.

CAA50226.1 X70881 Hordeum vulgare  
MybHv33. myb3.

CAA50223.1 X70878 Hordeum vulgare  
MybHv33. myb3.

CAA78387.1 Z13997 Petunia x hybrida  
DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb  
proto-oncoproteins.

CAA67000.1 X98355 Oryza sativa  
activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like;  
expression is regulated by gibberellin.

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AAK19616.1 AF336283 *Gossypium hirsutum*

GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.

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AAG28526.1 AF198499 *Nicotiana tabacum*

anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.

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CAA78386.1 Z13996 *Petunia x hybrida*

DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncogene. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.

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CAA66952.1 X98308 *Lycopersicon esculentum*

THM18. myb-related transcription factor.

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BAA23341.1 D88621 *Oryza sativa*

transfactor. OSMYB5. Osmyb5.

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CAA50221.1 X70876 *Hordeum vulgare*

MybHv5. myb2.

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AAK19611.1 AF336278 *Gossypium hirsutum*

BNLGH1233. bnlghi6233. similar to myb.

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AAC04716.1 AF034130 *Gossypium hirsutum*

putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-D. similar to MYB A encoded by GenBank Accession Number L04497.

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CAA61021.1 X87690 *Hordeum vulgare*

transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.

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AAG22863.1 AY008692 *Hordeum vulgare*

transcription factor GAMyb. Gamyb.

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SEQ ID NO: 767

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CAB08111.1 Z94180 *Lycopersicon esculentum*

branched chain alpha-keto acid dehydrogenase E1-alpha subunit.

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CAA81558.1 Z26949 *Solanum tuberosum*

subunit of the mitochondrial pyruvate dehydrogenase complex. E1 alpha subunit of pyruvate dehydrogenase precursor.

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AAC72195.1 AF069911 *Zea mays*

pyruvate dehydrogenase E1 alpha subunit.

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AAG43499.1 AF209924 *Lycopersicon esculentum*

pyruvate dehydrogenase.

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AAA97411.1 U51918 *Pisum sativum*

pyruvate dehydrogenase E1 alpha subunit.

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CAA10992.1 AJ222787 *Hordeum vulgare*

alpha-keto acid dehydrogenase-like protein. homology to branched chain alpha-keto acid dehydrogenase E1-alpha subunit.

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SEQ ID NO: 768

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AAF64450.1 AF239928 *Euphorbia esula*

glutathione S-transferase. similar to auxin-inducible GST.

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AAG16758.1 AY007560 *Lycopersicon esculentum*  
putative glutathione S-transferase T3.

AAG34803.1 AF243368 *Glycine max*  
glutathione S-transferase GST 13.

AAG16756.1 AY007558 *Lycopersicon esculentum*  
putative glutathione S-transferase T1.

AAG34796.1 AF243361 *Glycine max*  
glutathione S-transferase GST 6.

AAG34809.1 AF243374 *Glycine max*  
glutathione S-transferase GST 19.

AAG34797.1 AF243362 *Glycine max*  
glutathione S-transferase GST 7.

AAG34807.1 AF243372 *Glycine max*  
glutathione S-transferase GST 17.

AAG34798.1 AF243363 *Glycine max*  
glutathione S-transferase GST 8.

AAG34804.1 AF243369 *Glycine max*  
glutathione S-transferase GST 14.

AAG16759.1 AY007561 *Lycopersicon esculentum*  
putative glutathione S-transferase T4.

AAG34801.1 AF243366 *Glycine max*  
glutathione S-transferase GST 11.

AAG34810.1 AF243375 *Glycine max*  
glutathione S-transferase GST 20.

AAG16757.1 AY007559 *Lycopersicon esculentum*  
putative glutathione S-transferase T2.

AAC18566.1 AF048978 *Glycine max*  
2,4-D inducible glutathione S-transferase. GSTa.

AAG34808.1 AF243373 *Glycine max*  
glutathione S-transferase GST 18.

AAG34800.1 AF243365 *Glycine max*  
glutathione S-transferase GST 10.

CAA71784.1 Y10820 *Glycine max*  
glutathione transferase.

AAG34844.1 AF244701 *Zea mays*  
glutathione S-transferase GST 36.

AAG32472.1 AF309379 *Oryza sativa* subsp. *japonica*  
putative glutathione S-transferase OsGSTU3.

AAA68430.1 J03679 *Solanum tuberosum*  
glutathione S-transferase. gstd. previously called pathogenesis-related protein; prp1-1.

CAA04391.1 AJ000923 *Carica papaya*  
glutathione transferase. PGST1.

AAG34831.1 AF244688 Zea mays  
glutathione S-transferase GST 23.

CAA09187.1 AJ010448 Alopecurus myosuroides  
glutathione transferase. GST1a.

CAA09188.1 AJ010449 Alopecurus myosuroides  
glutathione transferase. GST1b.

AAG34802.1 AF243367 Glycine max  
glutathione S-transferase GST 12.

AAG34805.1 AF243370 Glycine max  
glutathione S-transferase GST 15.

AAG34832.1 AF244689 Zea mays  
glutathione S-transferase GST 24.

AAG34837.1 AF244694 Zea mays  
glutathione S-transferase GST 29.

AAG34836.1 AF244693 Zea mays  
glutathione S-transferase GST 28.

AAG32471.1 AF309378 Oryza sativa subsp. japonica  
putative glutathione S-transferase OsGSTU4.

AAG34849.1 AF244706 Zea mays  
glutathione S-transferase GST 41.

CAC24549.1 AJ296343 Cichorium intybus x Cichorium endivia  
glutathione S-transferase. chi-GST1. auxin-induced GST.

AAC32118.1 AF051214 Picea mariana  
probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione  
S-transferase encoded by GenBank Accession Number X56266.

AAG34795.1 AF243360 Glycine max  
glutathione S-transferase GST 5.

AAG34841.1 AF244698 Zea mays  
glutathione S-transferase GST 33.

AAF29773.1 AF159229 Gossypium hirsutum  
glutathione S-transferase. GST.

SEQ ID NO: 769

AAG34797.1 AF243362 Glycine max  
glutathione S-transferase GST 7.

AAG34798.1 AF243363 Glycine max  
glutathione S-transferase GST 8.

AAG34803.1 AF243368 Glycine max  
glutathione S-transferase GST 13.

AAG16758.1 AY007560 Lycopersicon esculentum  
putative glutathione S-transferase T3.

AAF64450.1 AF239928 Euphorbia esula  
glutathione S-transferase. similar to auxin-inducible GST.

AAG34801.1 AF243366 Glycine max  
glutathione S-transferase GST 11.

AAG34804.1 AF243369 Glycine max  
glutathione S-transferase GST 14.

AAG34796.1 AF243361 Glycine max  
glutathione S-transferase GST 6.

AAG34809.1 AF243374 Glycine max  
glutathione S-transferase GST 19.

AAG16759.1 AY007561 Lycopersicon esculentum  
putative glutathione S-transferase T4.

AAG16757.1 AY007559 Lycopersicon esculentum  
putative glutathione S-transferase T2.

AAG16756.1 AY007558 Lycopersicon esculentum  
putative glutathione S-transferase T1.

AAG34807.1 AF243372 Glycine max  
glutathione S-transferase GST 17.

AAG34810.1 AF243375 Glycine max  
glutathione S-transferase GST 20.

AAG34844.1 AF244701 Zea mays  
glutathione S-transferase GST 36.

AAG34831.1 AF244688 Zea mays  
glutathione S-transferase GST 23.

AAC18566.1 AF048978 Glycine max  
2,4-D inducible glutathione S-transferase. GSTa.

AAG34832.1 AF244689 Zea mays  
glutathione S-transferase GST 24.

AAG34808.1 AF243373 Glycine max  
glutathione S-transferase GST 18.

AAG34837.1 AF244694 Zea mays  
glutathione S-transferase GST 29.

AAG34800.1 AF243365 Glycine max  
glutathione S-transferase GST 10.

AAG34836.1 AF244693 Zea mays  
glutathione S-transferase GST 28.

CAA04391.1 AJ000923 Carica papaya  
glutathione transferase. PGST1.

CAA71784.1 Y10820 Glycine max  
glutathione transferase.

AAG34849.1 AF244706 Zea mays  
glutathione S-transferase GST 41.

AAA68430.1 J03679 Solanum tuberosum  
glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.

AAG34802.1	AF243367	Glycine max glutathione S-transferase GST 12.
CAC24549.1	AJ296343	Cichorium intybus x Cichorium endivia glutathione S-transferase. chi-GST1. auxin-induced GST.
CAA09187.1	AJ010448	Alopecurus myosuroides glutathione transferase. GST1a.
AAF22518.1	AF118925	Papaver somniferum glutathione S-transferase 2. GST2.
AAG32471.1	AF309378	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU4.
CAA09188.1	AJ010449	Alopecurus myosuroides glutathione transferase. GST1b.
AAF22517.1	AF118924	Papaver somniferum glutathione S-transferase 1. GST1.
AAF22647.1	AF193439	Lycopersicon esculentum glutathione S-transferase/peroxidase. BI-GST/GPX.
AAG32473.1	AF309380	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU2.
AAG32472.1	AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.
SEQ ID NO: 771		
AAG46118.1	AC073166	Oryza sativa putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
AAG13599.1	AC051633	Oryza sativa putative protein phosphatase-2C. OSJNBb0015I11.26.
BAB12036.1	AP002820	Oryza sativa putative protein phosphatase. P0702D12.18.
AAC36698.1	AF075580	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAA72341.1	Y11607	Medicago sativa protein phosphatase 2C. MP2C.
AAG43835.1	AF213455	Zea mays protein phosphatase type-2C. pp2c-1. PP2C-1.
CAB61839.1	AJ242803	Sporobolus stapfianus putative serine/threonine phosphatase type 2c.
AAD17804.1	AF092431	Lotus japonicus nodule-enhanced protein phosphatase type 2C. NPP2C1.
AAD17805.1	AF092432	Lotus japonicus protein phosphatase type 2C. PP2C2.
AAC36697.1	AF075579	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.

CAB90633.1 AJ277743 *Fagus sylvatica*  
protein phosphatase 2C (PP2C). pp2C1. ABA-induced protein.

CAC10358.1 AJ277086 *Nicotiana tabacum*  
protein phosphatase 2C. PP2C1.

CAC10359.1 AJ277087 *Nicotiana tabacum*  
protein phosphatase 2C. PP2C2.

AAC36700.1 AF075582 *Mesembryanthemum crystallinum*  
protein phosphatase-2C. PP2C.

CAC09575.1 AJ298987 *Fagus sylvatica*  
protein phosphatase 2C (PP2C). pp2Cf1.

AAK20060.1 AC025783 *Oryza sativa*  
putative protein phosphatase 2C. OSJNBa0001O14.1.

CAB90634.1 AJ277744 *Fagus sylvatica*  
protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.

AAC35951.1 AF079355 *Mesembryanthemum crystallinum*  
protein phosphatase-2c. PP2C.

AAD11430.1 AF097667 *Mesembryanthemum crystallinum*  
protein phosphatase 2C homolog. PP2C.

AAB93832.1 U81960 *Zea mays*  
kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.

AAC26828.1 AF075603 *Oryza sativa*  
kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.

AAC36699.1 AF075581 *Mesembryanthemum crystallinum*  
protein phosphatase-2C. PP2C.

CAC09576.1 AJ298988 *Fagus sylvatica*  
protein phosphatase 2C (PP2C). pp2Cf2.

SEQ ID NO: 777

AAD21872.1 AF078082 *Phaseolus vulgaris*  
receptor-like protein kinase homolog RK20-1.

AAB93834.1 U82481 *Zea mays*  
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

CAA74661.1 Y14285 *Brassica oleracea*  
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

AAD52097.1 AF088885 *Nicotiana tabacum*  
receptor-like kinase CHRK1. Chrk1.

CAA73134.1 Y12531 *Brassica oleracea*  
serine/threonine kinase. BRLK.

CAB41879.1	Y18260	Brassica oleracea
		SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea
		SRK5 protein. SRK5. receptor-like kinase.
AAA33008.1	M97667	Brassica napus
		serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus
		ser /thr kinase. S-locus receptor kinase. srk.
CAA67145.1	X98520	Brassica oleracea
		receptor-like kinase. SFR2.
AAA33000.1	M76647	Brassica oleracea
		receptor protein kinase. SKR6.
CAA73133.1	Y12530	Brassica oleracea
		serine /threonine kinase. ARLK.
AAA62232.1	U00443	Brassica napus
		S-receptor kinase. protein contains an immunoglobulin-like domain.
AAC23542.1	U20948	Ipomoea trifida
		receptor protein kinase. IRK1.
CAA74662.1	Y14286	Brassica oleracea
		SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAA92837.1	AB032474	Brassica oleracea
		S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa
		receptor protein kinase SRK12.
BAA23676.1	AB000970	Brassica rapa
		receptor kinase 1. BcRK1.
CAA79355.1	Z18921	Brassica oleracea
		S-receptor kinase-like protein.
BAB21001.1	AB054061	Brassica rapa
		S locus receptor kinase. SRK22.
BAA21132.1	D88193	Brassica rapa
		S-receptor kinase. SRK9 (B.c.).
BAA06285.1	D30049	Brassica rapa
		S-receptor kinase SRK9.
BAA92836.1	AB032473	Brassica oleracea
		S18 S-locus receptor kinase. SRK18.
BAA07576.1	D38563	Brassica rapa
		receptor protein kinase SRK8.
BAB18292.1	AP002860	Oryza sativa
		putative receptor-like protein kinase. P0409B08.19.
AAK21965.1	AY028699	Brassica napus
		receptor protein kinase PERK1.

BAA92954.1 AP001551 *Oryza sativa*  
Similar to *Oryza sativa* protein kinase (OSPK10) mRNA. (L27821).

BAB39873.1 AP002882 *Oryza sativa*  
putative protein kinase. P0439B06.8. contains ESTs  
AU056701(S20808),AU056702(S20808).

AAK00425.1 AC069324 *Oryza sativa*  
Putative protein kinase. OSJNBa0071K19.11.

BAB39435.1 AP003338 *Oryza sativa*  
putative receptor kinase. OJ1212\_B09.2.

BAB07904.1 AP002835 *Oryza sativa*  
putative S-receptor kinase. P0417G05.12.

BAA94518.1 AP001800 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome 2 section 111 of 255; putative receptor-like  
protein kinase (AC002392).

AAG16628.1 AY007545 *Brassica napus*  
protein serine/threonine kinase BNK1.

BAB39409.1 AP002901 *Oryza sativa*  
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

BAB16871.1 AP002537 *Oryza sativa*  
putative protein kinase APK1A *Arabidopsis thaliana*. P0001B06.24. contains ESTs  
C22608(R3192),D25110(R3192).

AAF91324.1 AF244890 *Glycine max*  
receptor-like protein kinase 3. RLK3. GmRLK3.

BAA82556.1 AB030083 *Populus nigra*  
lectin-like protein kinase. PnLPK.

AAF91323.1 AF244889 *Glycine max*  
receptor-like protein kinase 2. RLK2. GmRLK2.

AAF91322.1 AF244888 *Glycine max*  
receptor-like protein kinase 1. RLK1. GmRLK1.

SEQ ID NO: 779

AAK31284.1 AC079890 *Oryza sativa*  
putative quinone oxidoreductase. OSJNBb0089A17.10.

BAA78050.1 AB027757 *Cicer arietinum*  
NADPH oxidoreductase homolog.

BAA83082.1 AB030704 *Lithospermum erythrorhizon*  
LEDI-4 protein. LEDI-4. preferentially expressed in darkness; putative NADPH quinone  
oxidoreductase; similar to zeta-crystallin.

AAG53944.1 AF304461 *Triphysaria versicolor*  
quinone-oxidoreductase QR1. TvQR1.

SEQ ID NO: 780

AAK17067.1 AF254558 *Oryza sativa*  
NAC6. NAC6.

BAA89800.1 AB028185 Oryza sativa  
OsNAC6 protein. OsNAC6.

BAA89799.1 AB028184 Oryza sativa  
OsNAC5 protein. OsNAC5.

BAA89798.1 AB028183 Oryza sativa  
OsNAC4 protein. OsNAC4.

BAA89797.1 AB028182 Oryza sativa  
OsNAC3 protein. OsNAC3.

BAA89801.1 AB028186 Oryza sativa  
OsNAC7 protein. OsNAC7.

AAF68626.1 AF254124 Medicago truncatula  
NAC1. NAC1. NAC domain containing protein.

BAA89802.1 AB028187 Oryza sativa  
OsNAC8 protein. OsNAC8.

BAA78417.1 AB021178 Nicotiana tabacum  
NAC-domain protein. TERN. elicitor-responsive gene.

SEQ ID NO: 783

CAA54390.1 X77134 Brassica napus  
acyl-CoA binding protein.

CAA70200.1 Y08996 Ricinus communis  
acyl-CoA-binding protein.

CAB56693.1 AJ249833 Digitalis lanata  
binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp3.

CAB56694.1 AJ249834 Digitalis lanata  
binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp4.

AAB67736.1 U35015 Gossypium hirsutum  
acyl-CoA-binding protein.

AAB86851.1 AF031541 Fritillaria agrestis  
acyl-CoA-binding protein. acabp.

SEQ ID NO: 784

CAA58994.1 X84208 Sinapis alba  
trypsin inhibitor 2. mti-2.

CAA76116.1 Y16190 Sinapis alba  
trypsin inhibitor 2. mti-2.

SEQ ID NO: 785

AAF66242.1 AF243180 Lycopersicon esculentum  
dicyanin. binuclear blue copper protein; contains two stellacyanins linked together.

AAC32421.1	U65511	Cucumis sativus
putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Stellacyanins; similar to <i>Rhus vernicifera</i> stellacyanin: SwissProt Accession Number P00302; similar to <i>umecyanin</i> : SwissProt Accession Number P42849; similar to <i>mavicyanin</i> : SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number AF077407; glycoprotein.		
CAA80963.1	Z25471	Pisum sativum
blue copper protein.		
AAD10251.1	AF031195	Triticum aestivum
blue copper-binding protein homolog. S85.		
AAC64163.1	AF093537	Zea mays
blue copper protein. similar to pea blue copper protein in GenBank Accession Number Z25471.		
CAA10134.1	AJ012693	Cicer arietinum
basic blue copper protein.		
AAF66243.1	AF243181	Lycopersicon esculentum
plantacyanin. naturally occurring cupredoxin with a Val residue in the position of the axial ligand Met; member of the plantacyanin subfamily of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins.		
CAB65280.1	AJ248323	Medicago sativa subsp. x varia
basic blue protein. bab1.		
AAC32448.1	U76296	Spinacia oleracea
plantacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Plantacyanins; non-glycosylated.		
SEQ ID NO: 793		
BAA81862.1	AB026295	Oryza sativa
Similar to leucoanthocyanidin dioxygenase.(AI440611).		
AAB39995.1	U82432	Dianthus caryophyllus
anthocyanidin synthase. allele: S; 2-oxoglutarate-dependent dioxygenase.		
BAA36554.1	AB011796	Citrus unshiu
flavonol synthase. CitFLS.		
AAD56580.1	AF184273	Daucus carota
leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate dependent dioxygenase.		
AAD56581.1	AF184274	Daucus carota
leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate dependent dioxygenase.		
CAA50498.1	X71360	Malus sp.
anthocyanidin hydroxylase. apple equivalent to 'Candi' from <i>Antirrhinum majus</i> .		

AAD26205.1 AF117269 *Malus x domestica*  
anthocyanidin synthase. ANS.

AAB82287.1 AF026058 *Matthiola incana*  
anthocyanidin synthase.

CAA80264.1 Z22543 *Petunia x hybrida*  
flavonol synthase.

AAF64168.1 AF240764 *Eustoma grandiflorum*  
flavonol synthase. fls.

BAA20143.1 AB003779 *Perilla frutescens*  
leucoanthocyanidin dioxygenase.

AAB66560.1 AF015885 *Callistephus chinensis*  
anthocyanidin synthase.

BAB21477.1 AB044091 *Torenia fournieri*  
anthocyanidin synthase. 2-oxoglutarate dependent oxygenase.

CAA63092.1 X92178 *Solanum tuberosum*  
flavonol synthase.

AAD26261.1 AF119095 *Malus x domestica*  
flavonol synthase. FLS.

CAA53580.1 X75966 *Vitis vinifera*  
leucoanthocyanidin dioxygenase. LDOX.

BAA75305.1 AB023786 *Ipomoea batatas*  
anthocyanidin synthase. ans I.

AAB84049.1 AF028602 *Ipomoea purpurea*  
anthocyanidin synthase. ANS-FL1.

BAA75306.1 AB023787 *Ipomoea batatas*  
anthocyanidin synthase. ans II.

CAA73094.1 Y12489 *Forsythia x intermedia*  
anthocyanidin synthase.

CAA69252.1 Y07955 *Oryza sativa*  
anthocyanidin synthase. ANS.

SEQ ID NO: 794

AAD10204.1 AF030260 *Vicia sativa*  
CYP94A1. vagh111. cytochrome P450 fatty acid hydroxylase; Method: conceptual translation  
with partial peptide sequencing.

AAG33645.1 AF092917 *Vicia sativa*  
cytochrome P450-dependent fatty acid hydroxylase. CYP94A2.

AAG17470.1 AF123609 *Triticum aestivum*  
cytochrome P450.

BAA99523.1 AP002484 *Oryza sativa*  
putative cytochrome P450. P0489A01.14.

AAK31592.1 AY029178 *Brassica rapa subsp. pekinensis*  
cytochrome P450. mf-CYP450. possible relevance to male-sterility.

BAA99522.1 AP002484 *Oryza sativa*  
putative cytochrome P450. P0489A01.13.

BAA83370.1 AP000391 *Oryza sativa*  
ESTs AU056036(S20239),C72753(E2173), AU056035(S20239) correspond to a region of the predicted gene.; Similar to putative cytochrome P-450 (AC003680).

CAB41474.1 AJ238402 *Catharanthus roseus*  
cytochrome P450. CYP96C1.

AAB94586.1 AF022457 *Glycine max*  
CYP97B2p. CYP97B2. cytochrome P450 monooxygenase.

AAK20054.1 AC025783 *Oryza sativa*  
putative cytochrome P450 monooxygenase. OSJNBA0001O14.16.

AAK38086.1 AF321862 *Lolium rigidum*  
putative cytochrome P450.

AAK38085.1 AF321861 *Lolium rigidum*  
putative cytochrome P450.

AAB94588.1 AF022459 *Glycine max*  
CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

CAA89260.1 Z49263 *Pisum sativum*  
cytochrome P450.

AAG09208.1 AF175278 *Pisum sativum*  
wound-inducible P450 hydroxylase. CYP82A1.

AAC49188.2 U29333 *Pisum sativum*  
cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.

BAB19083.1 AP002744 *Oryza sativa*  
putative cytochrome P450. P0006C01.25. contains ESTs  
AU081507(C12518),C26520(C12518).

BAB19104.1 AP002839 *Oryza sativa*  
putative cytochrome P450. P0688A04.10. contains ESTs  
AU081507(C12518),C26520(C12518).

AAK38092.1 AF321868 *Lolium rigidum*  
putative cytochrome P450.

CAA04117.1 AJ000478 *Helianthus tuberosus*  
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-race).

AAK38091.1 AF321867 *Lolium rigidum*  
putative cytochrome P450.

CAA04116.1 AJ000477 *Helianthus tuberosus*  
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

BAA22423.1 AB001380 *Glycyrhiza echinata*  
cytochrome P450. CYP93B1.

CAA71876.1 Y10982 *Glycine max*  
putative cytochrome P450.

BAB39252.1 AP002968 *Oryza sativa*  
putative cytochrome P450. P0416G11.1.

AAA33106.1 L10081 *Catharanthus roseus*  
cytochrome P-450 protein. CYP72. putative; CYP72 protein.

AAA17746.1 L19075 *Catharanthus roseus*  
cytochrome P450. CYP72C. putative.

BAA74466.1 AB022733 *Glycyrrhiza echinata*  
cytochrome P450. CYP Ge-51.

BAB19121.1 AP002839 *Oryza sativa*  
putative cytochrome P450. P0688A04.28.

AAA17732.1 L19074 *Catharanthus roseus*  
cytochrome P450. CYP72B.

BAA93634.1 AB025016 *Lotus japonicus*  
cytochrome P450.

AAB05376.3 U35226 *Nicotiana plumbaginifolia*  
putative cytochrome P-450.

AAB61965.1 U48435 *Solanum chacoense*  
putative cytochrome P450.

AAF27282.1 AF122821 *Capsicum annuum*  
cytochrome P450. PepCYP.

CAB50768.1 AJ243804 *Cicer arietinum*  
putative isoflavone synthase. cytochrome P450. cyp93C3.

AAC34853.1 AF082028 *Hemerocallis* hybrid cultivar  
putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3.  
mRNA accumulates in senescing petals.

CAB43505.1 AJ239051 *Cicer arietinum*  
cytochrome P450. cyp81E2.

BAB21156.1 AP002899 *Oryza sativa*  
putative cytochrome P450. P0456A01.12.

CAA50648.1 X71657 *Solanum melongena*  
P450 hydroxylase.

BAB19112.1 AP002839 *Oryza sativa*  
putative cytochrome P450. P0688A04.18. contains ESTs  
AU067870(C10320),AU067869(C10320).

BAB19091.1 AP002744 *Oryza sativa*  
putative cytochrome P450. P0006C01.33. contains ESTs  
AU067870(C10320),AU067869(C10320).

BAA84072.1 AB028152 *Torenia hybrida*  
flavone synthase II. cytochrome P450. TFNS5.

BAA76380.1 AB023636 *Glycyrrhiza echinata*  
cytochrome P450. CYP Ge-8.

CAA72208.1 Y11404 *Zea mays*  
cytochrome p450. cyp71c2.

CAA57423.1	X81829	Zea mays
cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.		
BAB12433.1	AB025030	Coptis japonica
p450.		
SEQ ID NO: 798		
BAB21205.1	AP002913	Oryza sativa
nucleoid DNA-binding protein cnd41-like protein. P0480E02.11. contains ESTs		
AU166073(E31027),AU029516(E31027).		
BAA22813.1	D26015	Nicotiana tabacum
aspartic protease activity. CND41, chloroplast nucleoid DNA binding protein. cnd41.		
SEQ ID NO: 804		
AAD46491.1	AF135014	Zea mays
dihydrolipoamide S-acetyltransferase. pyruvate dehydrogenase complex E2 subunit.		
SEQ ID NO: 805		
BAA85412.1	AP000615	Oryza sativa
ESTs AU065232(E60855),C23624(S1554), AU078241(E60855) correspond to a region of the		
predicted gene.; similar to putative adenylate kinase. (AC005896).		
BAA01181.1	D10335	Oryza sativa
adenylate kinase-b. Adk-b.		
BAA01180.1	D10334	Oryza sativa
adenylate kinase-a. Adk-a.		
BAA94761.1	AB041773	Oryza sativa
adenylate kinase. Adk-a.		
AAB68604.1	U82330	Prunus armeniaca
adenylate kinase homolog.		
AAF23372.1	AF187063	Oryza sativa
catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or		
CDP. UMP/CMP kinase b. ura6.		
AAF23371.1	AF187062	Oryza sativa
catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or		
CDP. UMP/CMP kinase a. ura6.		
AAD41679.1	AF086603	Ceratopteris richardii
adenylate kinase. ADK1.		
BAA85443.1	AP000616	Oryza sativa
similar to UMP/CMP kinase (AF000147).		
SEQ ID NO: 808		
CAA41774.1	X59046	Oryza sativa
sucrose-UDP glucosyltransferase (isozyme 2). RSs2.		
BAA89049.1	AB029401	Citrus unshiu
sucrose synthase. CitSUS1-2.		
AAA34196.1	L19762	Lycopersicon esculentum
sucrose synthase.		

BAA88905.1	AB022092	Citrus unshiu sucrose synthase. CitSUS1.
AAD28641.1	U73588	Gossypium hirsutum sucrose synthase.
CAA49428.1	X69773	Vicia faba sucrose synthase. VfSucs.
AAC37346.1	M97551	Vicia faba cleavage of sucrose. UDP-glucose:D-fructose-2-glucosyltransferase. putative.
CAA09681.1	AJ011535	Lycopersicon esculentum sucrose synthase. sus2.
AAA97572.1	U24088	Solanum tuberosum sucrose synthase.
CAA09593.1	AJ011319	Lycopersicon esculentum sucrose synthase. sus3.
CAB40794.1	AJ131943	Medicago truncatula sucrose synthase. sucS1.
AAC17867.1	AF049487	Medicago sativa sucrose hydrolysis. sucrose synthase.
CAB40795.1	AJ131964	Medicago truncatula sucrose synthase. sucS1.
CAA65640.1	X96939	Tulipa gesneriana sucrose-synthase 21.
AAA97571.1	U24087	Solanum tuberosum sucrose synthase.
CAA63122.1	X92378	Alnus glutinosa sucrose synthase. sus1.
AAA33514.1	L22296	Zea mays UDP-glucose:D-fructose 2-glucosyl-transferase. Sus1.
CAA65639.1	X96938	Tulipa gesneriana sucrose-synthase 1.
AAC41682.1	L03366	Oryza sativa sucrose synthase 3. RSs3.
CAA75793.1	Y15802	Hordeum vulgare sucrose synthase 2. Ss2.
CAA49551.1	X69931	Hordeum vulgare sucrose synthase. Ss2.
CAA76056.1	Y16090	Daucus carota sucrose synthase isoform I. Susy*Dc1.
CAA53081.1	X75332	Daucus carota sucrose synthase.
AAA33515.1	L33244	Zea mays sucrose synthase 2. Sus1.

BAB20799.1 AB045710 *Pyrus pyrifolia*  
sucrose synthase 1. PypSUS1.

CAA03935.1 AJ000153 *Triticum aestivum*  
sucrose synthase type 2.

AAC39323.1 AF030231 *Glycine max*  
sucrose synthase. SS. nodulin-100.

BAA01108.1 D10266 *Vigna radiata*  
sucrose synthase. vss1.

CAA09910.1 AJ012080 *Pisum sativum*  
sucrose synthase.

AAC28107.1 AF079851 *Pisum sativum*  
nodule-enhanced sucrose synthase. ness.

CAC32462.1 AJ311496 *Pisum sativum*  
sucrose metabolism. sucrose synthase isoform 3. sus3.

CAA57881.1 X82504 *Chenopodium rubrum*  
sucrose synthase. CSS1.

CAA26229.1 X02382 *Zea mays*  
sucrose synthase.

CAA26247.1 X02400 *Zea mays*  
sucrose synthase.

CAA46017.1 X64770 *Oryza sativa*  
sucrose synthase. RSS1.

CAB38022.1 AJ132000 *Craterostigma plantagineum*  
sucrose metabolism. sucrose synthase. Ss2.

CAA78747.1 Z15028 *Oryza sativa*  
sucrose synthase.

AAF85966.1 AF263384 *Saccharum officinarum*  
sucrose synthase-1.

CAA46701.1 X65871 *Hordeum vulgare*  
sucrose synthase.

CAA04543.1 AJ001117 *Triticum aestivum*  
sucrose synthase type I. Ss1.

BAA88904.1 AB022091 *Citrus unshiu*  
sucrose synthase. CitSUSA.

BAA88981.1 AB025778 *Citrus unshiu*  
sucrose synthase. CitSUSA-2.

CAA04512.1 AJ001071 *Pisum sativum*  
second sucrose synthase.

CAA76057.1 Y16091 *Daucus carota*  
sucrose synthase isoform II. Susy\*Dc2.

CAB38021.1 AJ131999 *Craterostigma plantagineum*  
sucrose metabolism. sucrose synthase. Ss1.

CAA57499.1 X81974 Beta vulgaris  
sucrose synthase. SBSS1.

CAA47264.1 X66728 Hordeum vulgare  
sucrose synthase.

SEQ ID NO: 809

AAB69317.1 AF012861 Petroselinum crispum  
plastidic glucose-6-phosphate dehydrogenase. pG6PDH.

AAF87216.1 AF231351 Nicotiana tabacum  
plastidic glucose 6-phosphate dehydrogenase. G6PDHP2.

CAA67782.1 X99405 Nicotiana tabacum  
glucose-6-phosphate dehydrogenase. G6PD.

CAB52708.1 AJ010712 Solanum tuberosum  
glucose-6-phosphate 1-dehydrogenase. g6pd.

CAB52685.1 AJ132346 Dunaliella bioculata  
plastidic glucose-6-phosphate dehydrogenase. g6PD.

CAA58775.1 X83923 Solanum tuberosum  
glucose-6-phosphate dehydrogenase.

CAA03941.1 AJ000184 Spinacia oleracea  
Glucose-6-phosphate dehydrogenase. G6PD.

CAA03939.1 AJ000182 Spinacia oleracea  
Glucose-6-phosphate dehydrogenase. G6PD.

CAA04994.1 AJ001772 Nicotiana tabacum  
glucose-6-phosphate dehydrogenase. TCG18.

CAA03940.1 AJ000183 Spinacia oleracea  
Glucose-6-phosphate dehydrogenase. G6PD.

AAD11426.1 AF097663 Mesembryanthemum crystallinum  
cytoplasmic glucose-6-phosphate 1-dehydrogenase. G6PD.

AAB41552.1 U18238 Medicago sativa subsp. sativa  
glucose-6-phosphate dehydrogenase.

CAA52442.1 X74421 Solanum tuberosum  
glucose-6-phosphate 1-dehydrogenase. g6pdh. homotetramer.

AAB69318.1 AF012862 Petroselinum crispum  
cytosolic glucose-6-phosphate dehydrogenase 1. cG6PDH1.

AAB69319.1 AF012863 Petroselinum crispum  
cytosolic glucose-6-phosphate dehydrogenase 2. cG6PDH2.

CAA04992.1 AJ001769 Nicotiana tabacum  
glucose-6-phosphate dehydrogenase. TCG6.

CAA04993.1 AJ001770 Nicotiana tabacum  
glucose-6-phosphate dehydrogenase. TCG9.

BAA97662.1 AB029454 Triticum aestivum  
glucose-6-phosphate dehydrogenase. g6pdh.

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BAA97663.1 AB029455 *Triticum aestivum*  
glucose-6-phosphate dehydrogenase. g6pdh.

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BAA97664.1 AB029456 *Triticum aestivum*  
glucose-6-phosphate dehydrogenase. g6pdh.

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AAG23802.1 AF260736 *Cucurbita pepo*  
plastidic glucose-6-phosphate dehydrogenase.

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CAB66330.1 AJ279688 *Betula pendula*  
glucose-6-phosphate dehydrogenase. g6pd.

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BAA82155.1 AB011441 *Triticum aestivum*  
glucose-6-phosphate dehydrogenase. WESR5. salt-stress responding gene.

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CAA06200.1 AJ004900 *Glycine max*  
pentose phosphate pathway oxidoreductase generating NADPH. glucose-6-phosphate-dehydrogenase.

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SEQ ID NO: 812

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BAA08910.1 D50407 *Cucumis sativus*  
glutamyl-tRNA reductase. hemA.

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AAD16897.1 AF105221 *Glycine max*  
converts glutamyl-tRNA to glutamate 1-semialdehyde. glutamyl-tRNA reductase precursor. gtr1.

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BAA11091.1 D67088 *Cucumis sativus*  
glutamyl-tRNA reductase. hemA2.

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BAA25003.1 AB011416 *Oryza sativa*  
glutamyl-tRNA reductase.

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AAG13620.1 AC078840 *Oryza sativa*  
putative glutamyl-tRNA reductase. OSJNBb0073N24.1.

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CAA60054.1 X86101 *Hordeum vulgare*  
aminolevulinate synthesis (chlorophyll synthesis). glutamyl tRNA reductase. hemA 1. 1st isoform.

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CAA63140.1 X92403 *Hordeum vulgare*  
glutamyl-tRNA reductase. hemA1. isoform I.

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BAA25167.1 D88382 *Hordeum vulgare*  
glutamyl-tRNA reductase. hemA1. isoform 1.

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CAA60055.1 X86102 *Hordeum vulgare*  
aminolevulinate synthesis (chlorophyll synthesis). glutamyl tRNA reductase. hemA 2. 2nd isoform.

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BAA25168.1 D88383 *Hordeum vulgare*  
glutamyl-tRNA reductase. hemA3. isoform 3.

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AAG41962.1 AF305613 *Chlamydomonas reinhardtii*  
glutamyl-tRNA reductase precursor. HemA. pGtr.

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AAG02480.1 AF294753 *Hordeum vulgare*  
converts glutamyl-tRNA to glutamate 1-semialdehyde in the chlorophyll biosynthetic pathway. glutamyl-tRNA reductase. hemA2.

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AAG02479.1 AF294752 *Hordeum vulgare*  
 converts glutamyl-tRNA to glutamate 1-semialdehyde in the chlorophyll biosynthetic pathway. glutamyl-tRNA reductase. hemA1.

SEQ ID NO: 813

BAA82556.1 AB030083 *Populus nigra*  
 lectin-like protein kinase. PnLPK.

AAD21872.1 AF078082 *Phaseolus vulgaris*  
 receptor-like protein kinase homolog RK20-1.

AAF43408.1 AF230515 *Oryza sativa* subsp. *japonica*  
 serine/threonine protein kinase. YK35.

CAB51480.1 Y14600 *Sorghum bicolor*  
 putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

CAA73134.1 Y12531 *Brassica oleracea*  
 serine/threonine kinase. BRLK.

AAB93834.1 U82481 *Zea mays*  
 KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

AAK00425.1 AC069324 *Oryza sativa*  
 Putative protein kinase. OSJNBA0071K19.11.

BAA92954.1 AP001551 *Oryza sativa*  
 Similar to *Oryza sativa* protein kinase (OSPK10) mRNA. (L27821).

BAB39873.1 AP002882 *Oryza sativa*  
 putative protein kinase. P0439B06.8. contains ESTs  
 AU056701(S20808),AU056702(S20808).

BAB19337.1 AP003044 *Oryza sativa*  
 putative protein kinase. P0038C05.10. contains ESTs  
 AU056335(S20481),AU056336(S20481).

AAK21965.1 AY028699 *Brassica napus*  
 receptor protein kinase PERK1.

BAA92953.1 AP001551 *Oryza sativa*  
 Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).

BAB07906.1 AP002835 *Oryza sativa*  
 putative S-receptor kinase. P0417G05.14.

BAA94516.1 AP001800 *Oryza sativa*  
 Similar to *Zea mays* S-domain receptor-like protein kinase (AJ010166).

AAD52097.1 AF088885 *Nicotiana tabacum*  
 receptor-like kinase CHRK1. ChrK1.

BAB21240.1 AP002953 *Oryza sativa*  
 Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

AAC23542.1 U20948 *Ipomoea trifida*  
 receptor protein kinase. IRK1.

BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
AAA33915.1	L27821	Oryza sativa receptor type serine/threonine kinase. protein kinase.
BAB03429.1	AP002817	Oryza sativa EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAA94509.1	AB041503	Populus nigra protein kinase 1. PnPK1.
AAD46420.1	AF100771	Hordeum vulgare receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
AAD38286.1	AC007789	Oryza sativa putative protein kinase. OSJNBa0049B20.13.
BAB40081.1	AP003074	Oryza sativa putative receptor protein kinase. OSJNBa0004G10.30.
BAB18321.1	AP002865	Oryza sativa putative receptor protein kinase. P0034C11.11.
BAA94517.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c.).
BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
BAB07905.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.13.
BAA94529.2	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
AAB61708.1	U93048	Daucus carota somatic embryogenesis receptor-like kinase. SERK.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
AAK11674.1	AF339747	Lophopyrum elongatum protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.

BAA94528.1 AP001800 *Oryza sativa*  
 Similar to *Arabidopsis thaliana* chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).

BAA94510.1 AB041504 *Populus nigra*  
 protein kinase 2. PnPK2.

AAA33000.1 M76647 *Brassica oleracea*  
 receptor protein kinase. SKR6.

CAA67145.1 X98520 *Brassica oleracea*  
 receptor-like kinase. SFR2.

AAB47421.1 U59316 *Lycopersicon esculentum*  
 serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

BAA07577.2 D38564 *Brassica rapa*  
 receptor protein kinase SRK12.

AAA33008.1 M97667 *Brassica napus*  
 serine/threonine kinase receptor.

CAB89179.1 AJ245479 *Brassica napus* subsp. *napus*  
 ser /thr kinase. S-locus receptor kinase. srk.

BAA92837.1 AB032474 *Brassica oleracea*  
 S60 S-locus receptor kinase. SRK60.

SEQ ID NO: 814

AAF23903.1 AF194416 *Oryza sativa*  
 MAP kinase homolog. MAPK2. RMAPK2.

AAD52659.1 AF177392 *Oryza sativa*  
 blast and wounding induced mitogen-activated protein kinase. BWMK1. BWMK1 MAP kinase.

AAF23902.1 AF194415 *Oryza sativa*  
 MAP kinase homolog. MAPK1. RMAPK1.

AAD28617.1 AF129087 *Medicago sativa*  
 mitogen-activated protein kinase homologue. TDY1.

CAB61750.1 AJ275316 *Cicer arietinum*  
 MAP kinase protein.

AAB57843.1 U96716 *Selaginella lepidophylla*  
 MAP kinase-like protein. sdhn-6r.

AAF65766.1 AF242308 *Euphorbia esula*  
 mitogen-activated protein kinase. regulated by tyrosine and threonine phosphorylation.

BAB18271.1 AB035141 *Chlamydomonas reinhardtii*  
 mitogen-activated protein kinase. CrMPK2.

CAA58761.1 X83880 *Nicotiana tabacum*  
 p45Ntf4 serine/threonine protein kinase. ntf4.

CAA47099.1 X66469 *Medicago sativa*  
 MAP Kinase. MSK7.

AAB41548.1	L07042	Medicago sativa autophosphorylating serine/threonine protein kinase. MAP kinase. MsERK1.
AAB58396.1	U94192	Nicotiana tabacum salicylic acid-activated MAP kinase. NtSIPK.
CAA50036.1	X70703	Pisum sativum MAP kinase homologue. PSMAPKIN.
AAF73236.1	AF153061	Pisum sativum MAP kinase 3. Mapk3. PsMAPK3.
BAB32406.1	AB055515	Nicotiana tabacum NRK1 MAPK. nrk1. A tobacco MAPK that is phosphorylated and activated by NQK1.
CAA58760.1	X83879	Nicotiana tabacum p43Ntf6 serine/threonine protein kinase. ntf6.
CAA57721.1	X82270	Medicago sativa protein kinase. MMK4.
AAF81420.1	AF247136	Capsicum annuum MAP kinase 2. MK2. CAMK2; wound, UV-C, and cold-inducible expression.
AAD37790.1	AF149424	Ipomoea batatas MAP kinase.
AAG40580.1	AF216316	Oryza sativa MAP kinase 2. protein kinase; MAP2.
CAB37188.1	AJ224336	Medicago sativa MAP kinase. MMK3.
AAF61238.1	AF241166	Oryza sativa MAP kinase MAPK2.
AAG40581.1	AF216317	Oryza sativa MAP kinase 3. protein kinase; MAP3.
CAB61889.1	AJ251330	Oryza sativa protein kinase. MAPK4 protein. mapk4.
CAA73323.1	Y12785	Petroselinum crispum MAP kinase I.
CAC13967.1	AJ250311	Oryza sativa protein kinase. MAPK2 protein. mapk2.
CAA56314.1	X79993	Avena sativa MAP KINASE. Asmap1.
CAA49592.1	X69971	Nicotiana tabacum serine/threonine protein kinase. NTF3.
CAA58466.1	X83440	Petunia x hybrida MAP/ERK kinase 1. MEK1.
AAK01710.1	AF332873	Oryza sativa MAP kinase BIMK1.
AAG40579.1	AF216315	Oryza sativa MAP kinase 1. protein kinase; MAP1.

CAA57719.1	X82268	Medicago sativa protein kinase. MMK2.
AAC28850.1	AF079318	Triticum aestivum protein kinase. MAP kinase homolog. WCK-1.
AAD32204.1	AF134730	Prunus armeniaca putative mitogen-activated protein kinase MAPK. MAP kinase.
BAA74734.1	AB016802	Zea mays MAP kinase 5. ZmMPK5.
AAF73257.1	AF154329	Pisum sativum MAP kinase PsMAPK2. Mapk2.
BAA09600.1	D61377	Nicotiana tabacum WIPK. MAP (mitogen-activated protein) kinase.
AAF81419.1	AF247135	Capsicum annuum MAP kinase 1. MK1. wound and UV-C inducible expression.
BAA74733.1	AB016801	Zea mays MAP kinase 4. ZmMPK4.
CAA05328.1	AJ002314	Nicotiana tabacum serine/threonine protein kinase. shaggy-like kinase 111. NSK 111.
CAA05329.1	AJ002315	Nicotiana tabacum shaggy-like kinase 59. NSK 59.
CAA11861.1	AJ224164	Petunia x hybrida shaggy kinase 6. PSK6.
CAA58595.1	X83620	Petunia x hybrida Petunia Shaggy kinase 6. PSK6.
CAA11862.1	AJ224165	Petunia x hybrida shaggy kinase 7. PSK7.
CAA58594.1	X83619	Petunia x hybrida Petunia Shaggy kinase 4. PSK4.
AAA92823.1	U18365	Brassica napus cyclin dependent protein kinase homolog; similar to moth bean p34cdc2 protein, PIR Accession Number JQ2243.
BAA92214.1	AP001278	Oryza sativa ESTs C22403(C50132),C22404(C50132) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana shaggy related protein kinase ASK-gamma. (P43289).
CAA67554.1	X99100	Trifolium repens protein kinase. trK.

SEQ ID NO: 816

CAA65065.1	X95759	Solanum tuberosum glycogen (starch) synthase.
CAA64173.1	X94400	Solanum tuberosum soluble-starch-synthase. SSSIII.

AAC14014.1 AF023159 *Zea mays*  
starch synthase DULL1. dull1. similar to potato starch synthase SSIII; likely to be the maize starch synthase defined biochemically as SSII.

CAB40374.1 AJ225088 *Vigna unguiculata*  
ADP-glucose-starch glucosyltransferase. Starch synthase isoform SS III.

AAF88000.1 AF258609 *Aegilops tauschii*  
starch synthase III.

AAF87999.1 AF258608 *Triticum aestivum*  
starch synthase III. wSSIII.

CAB40375.1 AJ006752 *Vigna unguiculata*  
ADP-glucose starch glucosyltransferase. starch synthase, isoform V.

AAC14015.1 AF023160 *Zea mays*  
starch synthase DULL1. dull1. similar to potato starch synthase SSIII; like to be the maize starch synthase defined biochemically as SSII.

AAC17971.2 AF026422 *Chlamydomonas reinhardtii*  
soluble starch synthase. ADP-glucose:alpha-1, 4-D-glucan-4-alpha-D-glucosyltransferase.

AAD13342.1 AF019297 *Zea mays*  
starch synthase isoform zSTSII-2. zSSIIb.

CAB86618.1 AJ269502 *Triticum aestivum*  
transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-1. wSs2a-1.

CAA61269.1 X88790 *Pisum sativum*  
glycogen (starch) synthase.

CAB96626.1 AJ269503 *Triticum aestivum*  
transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-2. wSs2a-2.

CAB96627.1 AJ269504 *Triticum aestivum*  
transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-3. wSs2a-3.

CAA71442.1 Y10416 *Solanum tuberosum*  
soluble starch (bacterial glycogen) synthase. SS I.

AAD53263.1 AF155217 *Triticum aestivum*  
starch synthase IIa.

AAF37876.1 AF234163 *Hordeum vulgare*  
starch synthase I. SSI.

CAB99209.1 AJ292521 *Triticum aestivum*  
essential for starch synthesis. starch synthase I-1. wSsI-1.

AAD54661.1 AF091803 *Triticum aestivum*  
starch synthase I.

AAB17085.1 U66377 *Triticum aestivum*  
starch synthase. TaSS. EC 2.4.1.11.

CAB99210.1 AJ292522 *Triticum aestivum*  
essential for starch synthesis. starch synthase I-2. wSsI-2.

AAF03557.1 AF091802 *Aegilops tauschii*  
starch synthase I.

AAD13341.1 AF019296 *Zea mays*  
starch synthase isoform zSTSII-1. zSSIIa.

AAC17969.2 AF026420 *Chlamydomonas reinhardtii*  
ADP-Glucose:alpha-1, 4-D-glucan-4-alpha-D-glucosyltransferase. granule-bound starch synthase I precursor. STA2. GBSSI.

BAA82346.1 AB029546 *Phaseolus vulgaris*  
granule-bound starch synthase I. GBSSI.

CAA37732.1 X53694 *Oryza sativa*  
starch synthase.

CAA52273.1 X74160 *Manihot esculenta*  
starch (bacterial glycogen) synthase. GBSS.

AAF72561.1 AF141954 *Oryza sativa*  
granule-bound starch synthase. Waxy.

CAA46294.1 X65183 *Oryza sativa*  
glycogen (starch) synthase. waxy gene. starch granule enzyme.

AAF72562.1 AF141955 *Oryza sativa*  
granule-bound starch synthase. Waxy.

CAA44065.1 X62134 *Oryza sativa*  
starch biosynthesis. starch (bacterial glycogen) synthase. Wx.

AAB02197.1 U48227 *Triticum aestivum*  
soluble starch synthase.

AAF13168.1 AF173900 *Manihot esculenta*  
granule bound starch synthase II precursor. GBSSII. MEGBSSII.

CAA45472.1 X64108 *Oryza sativa*  
starch granule-bound starch synthase. waxy.

AAC61675.2 AF031162 *Oryza sativa*  
granule-bound starch synthase. Waxy.

AAC70779.1 AF097922 *Astragalus membranaceus*  
granule-bound glycogen (starch) synthase. GBSS.

CAA06958.1 AJ006293 *Antirrhinum majus*  
granule-bound starch synthase. waxy.

AAC19119.1 AF068834 *Ipomoea batatas*  
starch synthase.

AAD49850.1 AF165890 *Oryza sativa* subsp. *japonica*  
soluble starch synthase.

BAA81848.1 AB026295 *Oryza sativa*  
ESTs AU075322(C11109),D22430(C11109) correspond to a region of the predicted gene.;  
Rice gene for soluble starch synthase (SSS1), complete cds (exon1-15).(D38221).

BAA03739.1 D16202 *Oryza sativa*  
soluble starch synthase precursor.

CAA61268.1	X88789	Pisum sativum glycogen (starch) synthase.
AAA86423.1	U44126	Ipomoea batatas starch synthase. SPSS67.
AAF14233.1	AF109395	Triticum aestivum granule-bound starch synthase GBSSII.
CAA41359.1	X58453	Solanum tuberosum glycogen (starch) synthase. amf. waxy protein, granule-bound starch synthase.
AAG43519.1	AF210699	Perilla frutescens granule-bound starch synthase. GBSSI. waxy protein.
		SEQ ID NO: 819
BAA13032.1	D86180	Pisum sativum phosphoribosylanthranilate transferase. PAT1.
		SEQ ID NO: 822
AAB86850.1	AF031540	Fritillaria agrestis cytochrome C. cytC.
AAC84135.1	AF101422	Cichorium intybus cytochrome.
BAA02159.1	D12634	Oryza sativa 'cytochrome C'.
AAA63515.1	M63704	Oryza sativa cytochrome c. Cc-1.
AAA92712.1	L77113	Helianthus annuus cytochrome c. cytc1. putative.
AAB70265.1	AF017367	Oryza sativa cytochrome C.
AAA33084.1	M35173	Chlamydomonas reinhardtii apocytochrome c (cyc).
CAB16954.1	Z99829	Chlamydomonas reinhardtii cytochrome c. CYC1.
CAA79708.1	Z21499	Stellaria longipes mitochondrial cytochrome c.
		SEQ ID NO: 823
BAA02159.1	D12634	Oryza sativa 'cytochrome C'.
AAA63515.1	M63704	Oryza sativa cytochrome c. Cc-1.
AAB86850.1	AF031540	Fritillaria agrestis cytochrome C. cytC.
AAC84135.1	AF101422	Cichorium intybus cytochrome.

AAA92712.1 L77113 *Helianthus annuus*  
cytochrome c. cytcl. putative.

AAB70265.1 AF017367 *Oryza sativa*  
cytochrome C.

AAA33084.1 M35173 *Chlamydomonas reinhardtii*  
apocytochrome c (cyc).

CAB16954.1 Z99829 *Chlamydomonas reinhardtii*  
cytochrome c. CYC1.

CAA79708.1 Z21499 *Stellaria longipes*  
mitochondrial cytochrome c.

SEQ ID NO: 825

BAB17113.1 AP002866 *Oryza sativa*  
putative white protein; ATP-binding cassette transporter. P0410E01.34.

AAF43869.1 AF166114 *Chloroplast Mesostigma viride*  
probable transport protein. cysA.

BAA90508.1 AP001111 *Oryza sativa*  
similar to ABC transporter of *Arabidopsis thaliana* (AC004697).

AAD54843.1 AF137379 *Chloroplast Nephroselmis olivacea*  
probable transport protein. cysA.

BAA57907.1 AB001684 *Chlorella vulgaris*  
sulfate transport system permease protein. cysA.

BAA90507.1 AP001111 *Oryza sativa*  
similar to ABC transporter of *Arabidopsis thaliana* (AC004697).

BAB40032.1 AP003046 *Oryza sativa*  
putative ABC transporter. P0445D12.3.

AAG49003.1 AY013246 *Hordeum vulgare*  
putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.

BAB21275.1 AP002844 *Oryza sativa*  
putative ABC transporter protein. P0410E03.6.

AAG45492.1 AY013245 *Oryza sativa*  
36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.

AAG49002.1 AY013246 *Hordeum vulgare*  
putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.

BAB21276.1 AP002844 *Oryza sativa*  
putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).

AAD10836.1 U52079 *Solanum tuberosum*  
P-glycoprotein. pmdrl. binds ATP; ATPase; transporter; transmembrane protein.

BAB21279.1 AP002844 *Oryza sativa*  
putative ABC transporter protein. P0410E03.10. contains ESTs  
AU065360(R3463),AU101680(R3463).

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BAB21273.1 AP002844 Oryza sativa  
putative ABC transporter protein. P0410E03.4.

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BAA83352.1 AP000391 Oryza sativa  
ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.;  
Similar to ABC transporter-7 (U43892).

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BAA96612.1 AP002482 Oryza sativa  
Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter  
(AC004411).

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SEQ ID NO: 827

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AAG34803.1 AF243368 Glycine max  
glutathione S-transferase GST 13.

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AAG16758.1 AY007560 Lycopersicon esculentum  
putative glutathione S-transferase T3.

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AAG34798.1 AF243363 Glycine max  
glutathione S-transferase GST 8.

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AAF64450.1 AF239928 Euphorbia esula  
glutathione S-transferase. similar to auxin-inducible GST.

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AAG34807.1 AF243372 Glycine max  
glutathione S-transferase GST 17.

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AAG34796.1 AF243361 Glycine max  
glutathione S-transferase GST 6.

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AAG16759.1 AY007561 Lycopersicon esculentum  
putative glutathione S-transferase T4.

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AAG34797.1 AF243362 Glycine max  
glutathione S-transferase GST 7.

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AAG34801.1 AF243366 Glycine max  
glutathione S-transferase GST 11.

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AAG34804.1 AF243369 Glycine max  
glutathione S-transferase GST 14.

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AAG34809.1 AF243374 Glycine max  
glutathione S-transferase GST 19.

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AAG34808.1 AF243373 Glycine max  
glutathione S-transferase GST 18.

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AAG34810.1 AF243375 Glycine max  
glutathione S-transferase GST 20.

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AAG16757.1 AY007559 Lycopersicon esculentum  
putative glutathione S-transferase T2.

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AAG16756.1 AY007558 Lycopersicon esculentum  
putative glutathione S-transferase T1.

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AAG34844.1 AF244701 Zea mays  
glutathione S-transferase GST 36.

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AAG34805.1 AF243370 Glycine max  
glutathione S-transferase GST 15.

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AAG34831.1 AF244688 Zea mays  
glutathione S-transferase GST 23.

AAG34832.1 AF244689 Zea mays  
glutathione S-transferase GST 24.

AAG34849.1 AF244706 Zea mays  
glutathione S-transferase GST 41.

AAG34802.1 AF243367 Glycine max  
glutathione S-transferase GST 12.

CAA09187.1 AJ010448 Alopecurus myosuroides  
glutathione transferase. GST1a.

AAG34829.1 AF244686 Zea mays  
glutathione S-transferase GST 21.

CAA09188.1 AJ010449 Alopecurus myosuroides  
glutathione transferase. GST1b.

AAA68430.1 J03679 Solanum tuberosum  
glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.

AAG34836.1 AF244693 Zea mays  
glutathione S-transferase GST 28.

AAG34837.1 AF244694 Zea mays  
glutathione S-transferase GST 29.

AAG34800.1 AF243365 Glycine max  
glutathione S-transferase GST 10.

AAC18566.1 AF048978 Glycine max  
2,4-D inducible glutathione S-transferase. GSTa.

AAC32118.1 AF051214 Picea mariana  
probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.

AAF22517.1 AF118924 Papaver somniferum  
glutathione S-transferase 1. GST1.

AAF22518.1 AF118925 Papaver somniferum  
glutathione S-transferase 2. GST2.

AAG32471.1 AF309378 Oryza sativa subsp. japonica  
putative glutathione S-transferase OsGSTU4.

AAG34806.1 AF243371 Glycine max  
glutathione S-transferase GST 16.

CAA04391.1 AJ000923 Carica papaya  
glutathione transferase. PGST1.

AAG32472.1 AF309379 Oryza sativa subsp. japonica  
putative glutathione S-transferase OsGSTU3.

AAG34833.1 AF244690 Zea mays  
glutathione S-transferase GST 25.

CAA71784.1 Y10820 Glycine max  
glutathione transferase.

AAG34847.1 AF244704 Zea mays  
glutathione S-transferase GST 39.

AAF22519.1 AF118926 Papaver somniferum  
glutathione S-transferase 3. GST3.

SEQ ID NO: 828

AAG34803.1 AF243368 Glycine max  
glutathione S-transferase GST 13.

AAG34797.1 AF243362 Glycine max  
glutathione S-transferase GST 7.

AAG34798.1 AF243363 Glycine max  
glutathione S-transferase GST 8.

AAF64450.1 AF239928 Euphorbia esula  
glutathione S-transferase. similar to auxin-inducible GST.

AAG16758.1 AY007560 Lycopersicon esculentum  
putative glutathione S-transferase T3.

AAG34796.1 AF243361 Glycine max  
glutathione S-transferase GST 6.

AAG16759.1 AY007561 Lycopersicon esculentum  
putative glutathione S-transferase T4.

AAG34801.1 AF243366 Glycine max  
glutathione S-transferase GST 11.

AAG34804.1 AF243369 Glycine max  
glutathione S-transferase GST 14.

AAG34807.1 AF243372 Glycine max  
glutathione S-transferase GST 17.

AAG34809.1 AF243374 Glycine max  
glutathione S-transferase GST 19.

AAG34810.1 AF243375 Glycine max  
glutathione S-transferase GST 20.

AAG16757.1 AY007559 Lycopersicon esculentum  
putative glutathione S-transferase T2.

AAG16756.1 AY007558 Lycopersicon esculentum  
putative glutathione S-transferase T1.

AAG34802.1 AF243367 Glycine max  
glutathione S-transferase GST 12.

AAG34808.1 AF243373 Glycine max  
glutathione S-transferase GST 18.

AAG34844.1 AF244701 Zea mays  
glutathione S-transferase GST 36.

CAA09188.1 AJ010449 Alopecurus myosuroides  
glutathione transferase. GST1b.

CAA09187.1	AJ010448	Alopecurus myosuroides glutathione transferase. GST1a.
AAG32472.1	AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.
AAA68430.1	J03679	Solanum tuberosum glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
AAG34837.1	AF244694	Zea mays glutathione S-transferase GST 29.
AAG34800.1	AF243365	Glycine max glutathione S-transferase GST 10.
AAG34831.1	AF244688	Zea mays glutathione S-transferase GST 23.
AAC32118.1	AF051214	Picea mariana probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG34805.1	AF243370	Glycine max glutathione S-transferase GST 15.
AAC18566.1	AF048978	Glycine max 2,4-D inducible glutathione S-transferase. GSTa.
AAG34829.1	AF244686	Zea mays glutathione S-transferase GST 21.
CAA04391.1	AJ000923	Carica papaya glutathione transferase. PGST1.
CAA71784.1	Y10820	Glycine max glutathione transferase.
AAG34795.1	AF243360	Glycine max glutathione S-transferase GST 5.
AAG34836.1	AF244693	Zea mays glutathione S-transferase GST 28.
AAG34832.1	AF244689	Zea mays glutathione S-transferase GST 24.
AAG34833.1	AF244690	Zea mays glutathione S-transferase GST 25.
AAG34849.1	AF244706	Zea mays glutathione S-transferase GST 41.
AAG34806.1	AF243371	Glycine max glutathione S-transferase GST 16.
CAA09189.1	AJ010450	Alopecurus myosuroides glutathione transferase. GST1c.
SEQ ID NO: 829		
AAG34803.1	AF243368	Glycine max glutathione S-transferase GST 13.

AAF64450.1 AF239928 *Euphorbia esula*  
glutathione S-transferase. similar to auxin-inducible GST.

AAG16758.1 AY007560 *Lycopersicon esculentum*  
putative glutathione S-transferase T3.

AAG34798.1 AF243363 *Glycine max*  
glutathione S-transferase GST 8.

AAG34801.1 AF243366 *Glycine max*  
glutathione S-transferase GST 11.

AAG34797.1 AF243362 *Glycine max*  
glutathione S-transferase GST 7.

AAG34796.1 AF243361 *Glycine max*  
glutathione S-transferase GST 6.

AAG34807.1 AF243372 *Glycine max*  
glutathione S-transferase GST 17.

AAG16759.1 AY007561 *Lycopersicon esculentum*  
putative glutathione S-transferase T4.

AAG34804.1 AF243369 *Glycine max*  
glutathione S-transferase GST 14.

AAG34810.1 AF243375 *Glycine max*  
glutathione S-transferase GST 20.

AAG34809.1 AF243374 *Glycine max*  
glutathione S-transferase GST 19.

AAG16757.1 AY007559 *Lycopersicon esculentum*  
putative glutathione S-transferase T2.

AAG16756.1 AY007558 *Lycopersicon esculentum*  
putative glutathione S-transferase T1.

AAG34805.1 AF243370 *Glycine max*  
glutathione S-transferase GST 15.

AAC18566.1 AF048978 *Glycine max*  
2,4-D inducible glutathione S-transferase. GSTa.

AAG34808.1 AF243373 *Glycine max*  
glutathione S-transferase GST 18.

AAG34800.1 AF243365 *Glycine max*  
glutathione S-transferase GST 10.

AAG34829.1 AF244686 *Zea mays*  
glutathione S-transferase GST 21.

AAG34802.1 AF243367 *Glycine max*  
glutathione S-transferase GST 12.

AAG34837.1 AF244694 *Zea mays*  
glutathione S-transferase GST 29.

CAA09187.1 AJ010448 *Alopecurus myosuroides*  
glutathione transferase. GST1a.

CAA09188.1	AJ010449	Alopecurus myosuroides glutathione transferase. GST1b.
AAG34849.1	AF244706	Zea mays glutathione S-transferase GST 41.
AAG34844.1	AF244701	Zea mays glutathione S-transferase GST 36.
AAG34806.1	AF243371	Glycine max glutathione S-transferase GST 16.
CAA71784.1	Y10820	Glycine max glutathione transferase.
AAA68430.1	J03679	Solanum tuberosum glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
CAA04391.1	AJ000923	Carica papaya glutathione transferase. PGST1.
AAG34836.1	AF244693	Zea mays glutathione S-transferase GST 28.
AAG34831.1	AF244688	Zea mays glutathione S-transferase GST 23.
AAG34847.1	AF244704	Zea mays glutathione S-transferase GST 39.
AAC32118.1	AF051214	Picea mariana probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAF29773.1	AF159229	Gossypium hirsutum glutathione S-transferase. GST.
AAG32472.1	AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.
AAG41204.1	AF321437	Suaeda maritima glutathione transferase.
CAC24549.1	AJ296343	Cichorium intybus x Cichorium endivia glutathione S-transferase. chi-GST1. auxin-induced GST.
SEQ ID NO: 830		
AAD37699.1	AF145730	Oryza sativa homeodomain leucine zipper protein. Oshox6. transcription factor.
BAA93461.1	AB028073	Physcomitrella patens homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.
AAF01765.1	AF184278	Glycine max homeodomain-leucine zipper protein 57. Hdl57. transcription factor.
AAF01764.2	AF184277	Glycine max homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
BAA93466.1	AB028078	Physcomitrella patens homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.

CAB67118.1	Y17306	<i>Lycopersicon esculentum</i> homeodomain protein. h52.
AAF73482.1	AF268422	<i>Brassica rapa</i> subsp. <i>pekinensis</i> hb-6-like protein. transcription factor; similar to <i>Arabidopsis thaliana</i> hb-6 protein.
AAD37697.1	AF145728	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox4. transcription factor.
BAA21017.1	D26578	<i>Daucus carota</i> transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.
BAA05624.1	D26575	<i>Daucus carota</i> transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.
BAA93460.1	AB028072	<i>Physcomitrella patens</i> homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.
BAA93464.1	AB028076	<i>Physcomitrella patens</i> homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.
BAA93467.1	AB028079	<i>Physcomitrella patens</i> homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.
BAA93465.1	AB028077	<i>Physcomitrella patens</i> homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.
BAA05625.1	D26576	<i>Daucus carota</i> transcriptiional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.
BAA93468.1	AB028080	<i>Physcomitrella patens</i> homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA05623.1	D26574	<i>Daucus carota</i> tranciptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
BAA05622.1	D26573	<i>Daucus carota</i> transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.
AAD37698.1	AF145729	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox5. transcription factor.
CAA64221.1	X94449	<i>Pimpinella brachycarpa</i> transcription activator. homeobox-leucine zipper protein. PHZ4.
CAA64152.1	X94375	<i>Pimpinella brachycarpa</i> transcription activator. homeobox-leucine zipper protein.
CAA64491.1	X95193	<i>Pimpinella brachycarpa</i> transcription activator. homeobox-leucine zipper protein.
BAA93463.1	AB028075	<i>Physcomitrella patens</i> homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA06728.1	AJ005833	<i>Craterostigma plantagineum</i> transcription factor. homeodomain leucine zipper protein. hb-2.

AAD37695.1	AF145726	Oryza sativa
		homeodomain leucine zipper protein. Oshox2. transcription factor.
CAA65456.2	X96681	Oryza sativa
		transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	Oryza sativa
		homeodomain-leucine zipper transcription factor. Hox1. hox1.
AAK31270.1	AC079890	Oryza sativa
		homeodomain leucine zipper protein hox1. OSJNBb0089A17.12.
CAA63222.1	X92489	Glycine max
		transcription activator. homeobox-leucine zipper protein.
CAA06717.1	AJ005820	Craterostigma plantagineum
		transcription factor. homeodomain leucine zipper protein. hb-1.
AAA79778.1	L48485	Helianthus annuus
		homeodomain protein. putative.
		SEQ ID NO: 831
CAA06334.1	AJ005077	Lycopersicon esculentum
		protein kinase. TCTR2 protein. TCTR2.
AAG31141.1	AF305911	Oryza sativa
		EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAG31142.1	AF305912	Hordeum vulgare
		EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAK30005.1	AY029067	Rosa hybrid cultivar
		CTR2 protein kinase.
AAD46406.1	AF096250	Lycopersicon esculentum
		ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
CAA73722.1	Y13273	Lycopersicon esculentum
		putative protein kinase.
AAD10057.1	AF110519	Lycopersicon esculentum
		ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
AAD10056.1	AF110518	Lycopersicon esculentum
		ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
AAA34002.1	M67449	Glycine max
		protein kinase. PK6.
AAK11734.1	AY027437	Arachis hypogaea
		serine/threonine/tyrosine kinase.
BAB16918.1	AP002863	Oryza sativa
		putative protein kinase. P0005A05.22.
CAC09580.1	AJ298992	Fagus sylvatica
		Abscisic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAF59906.1	AF197947	Glycine max receptor protein kinase-like protein. CLV1B.
AAF59905.1	AF197946	Glycine max receptor protein kinase-like protein. CLV1A.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAA87852.1	AP000816	Oryza sativa Similar to putative Ser/Thr protein kinase. (AC004218).
BAB40094.1	AP003210	Oryza sativa putative receptor protein kinase. OSJNBa0010K01.7.
BAA92221.1	AP001278	Oryza sativa Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
CAA08995.1	AJ010091	Brassica napus MAP3K alpha 1 protein kinase. MAP3K alpha 1.
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
CAB51834.1	00069	Oryza sativa I1332.5. contains eukaryotic protein kinase domain PF.
CAA08997.1	AJ010093	Brassica napus MAP3K beta 1 protein kinase. MAP3K beta 1.
CAB54520.1	AJ238845	Brassica napus putative role in cell cycle control. MAP3K epsilon 1 protein kinase. MAP3K $\epsilon$ 1.
AAF34436.1	AF172282	Oryza sativa similar to mitogen-activated protein kinases. DUPR11.32.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAG25966.1	AF302082	Nicotiana tabacum cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
BAA06538.1	D31737	Nicotiana tabacum protein-serine/threonine kinase.
AAF76189.1	AF271206	Rosa hybrid cultivar CTR1-like protein kinase. Raf-like protein kinase.
BAA84787.1	AP000559	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

BAA83373.1	AP000391	Oryza sativa
ESTs C22657(S0014), C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).		
AAF66615.1	AF142596	Nicotiana tabacum
LRR receptor-like protein kinase.		
AAF91322.1	AF244888	Glycine max
receptor-like protein kinase 1. RLK1. GmRLK1.		
AAD21872.1	AF078082	Phaseolus vulgaris
receptor-like protein kinase homolog RK20-1.		
CAA61510.1	X89226	Oryza sativa
leucine-rich repeat/receptor protein kinase. Irk2.		
BAA87853.1	AP000816	Oryza sativa
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).		
AAF91323.1	AF244889	Glycine max
receptor-like protein kinase 2. RLK2. GmRLK2.		
AAF91324.1	AF244890	Glycine max
receptor-like protein kinase 3. RLK3. GmRLK3.		
AAF43394.1	AF230501	Oryza sativa subsp. japonica
serine/threonine protein kinase. YK1.		
AAK16409.1	AF320086	Zea mays
serine threonine kinase 1. stk1. expressed in mature tassel.		
AAK21965.1	AY028699	Brassica napus
receptor protein kinase PERK1.		
BAB39437.1	AP003338	Oryza sativa
receptor-like kinase. OJ1212_B09.6.		
AAK11568.1	AF318492	Lycopersicon hirsutum
Pto-like protein kinase B. LhirPtoB.		
SEQ ID NO: 832		
AAF35901.1	AF230332	Zinnia elegans
expansin 2.		
CAC19184.1	AJ291817	Cicer arietinum
expansin.		
AAG13982.1	AF297521	Prunus avium
expansin 1. Exp1. PruavExp1.		
BAB19676.1	AB029083	Prunus persica
expansin. PchExp1.		
AAC33529.1	U93167	Prunus armeniaca
expansin. PA-Exp1.		
AAC33530.1	AF038815	Prunus armeniaca
expansin. Exp2.		
AAD47901.1	AF085330	Pinus taeda
expansin.		

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AAB37746.1 U30382 *Cucumis sativus*  
expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.

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AAF21101.1 AF159563 *Fragaria x ananassa*  
expansin. Exp2. ripening regulated.

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AAB40634.1 U64890 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

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AAB40637.1 U64893 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

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AAB40635.1 U64891 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

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CAB43197.1 AJ239068 *Lycopersicon esculentum*  
cell wall loosening enzyme. expansin2. exp2.

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AAB40636.1 U64892 *Pinus taeda*  
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

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AAC64201.1 AF096776 *Lycopersicon esculentum*  
expansin. LeEXP2.

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AAD49956.1 AF167360 *Rumex palustris*  
expansin. EXP1.

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AAC96081.1 AF049354 *Nicotiana tabacum*  
involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.

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AAC39512.1 AF043284 *Gossypium hirsutum*  
expansin. GhEXP1. contains N-terminal signal peptide.

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AAB81662.1 U85246 *Oryza sativa*  
expansin. Os-EXP4.

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AAG13983.1 AF297522 *Prunus avium*  
expansin 2. Exp2. PruavExp2.

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AAF32409.1 AF230276 *Triphysaria versicolor*  
alpha-expansin 3.

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AAG32921.1 AF184233 *Lycopersicon esculentum*  
expansin. Exp10.

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BAB32732.1	AB049406	Eustoma grandiflorum expansin. Eg Expansin.
AAF32411.1	AF230278	Triphysaria versicolor alpha-expansin 1.
AAF35902.1	AF230333	Zinnia elegans expansin 3.
AAB38074.1	U30477	Oryza sativa induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.
AAC96080.1	AF049353	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.
AAF17570.1	AF202119	Marsilea quadrifolia alpha-expansin. EXP1. Mq-EXP1.
CAC06433.1	AJ276007	Festuca pratensis expansin. exp2.
AAD13633.1	AF059489	Lycopersicon esculentum expansin precursor. Exp5.
CAC19183.1	AJ291816	Cicer arietinum expansin.
AAF62181.1	AF247163	Oryza sativa alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAF62180.1	AF247162	Oryza sativa alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
CAB46492.1	AJ243340	Lycopersicon esculentum expansin9. exp9.
BAA88200.1	AP000837	Oryza sativa EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAF32410.1	AF230277	Triphysaria versicolor alpha-expansin 2.
AAB37749.1	U30460	Cucumis sativus expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
CAA04385.1	AJ000885	Brassica napus Cell wall extension in plants. Expansin.
AAF17571.1	AF202120	Regnellidium diphyllum alpha-expansin. EXP1. Rd-EXP1.
AAD13632.1	AF059488	Lycopersicon esculentum expansin precursor. Exp4.
CAA06271.2	AJ004997	Lycopersicon esculentum expansin18. exp18.

AAC63088.1	U82123	<i>Lycopersicon esculentum</i> expansin. LeEXP1. fruit ripening regulated expansin.
AAC96077.1	AF049350	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAF62182.1	AF247164	<i>Oryza sativa</i> alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
CAC18802.1	AJ289154	<i>Glycine max</i> expansion of cell walls. expansin. dd2/63.
AAC96078.1	AF049351	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAG01875.1	AF291659	<i>Striga asiatica</i> alpha-expansin 3. Exp3.
CAA69105.1	Y07782	<i>Oryza sativa</i> expansin. RiExA.
AAC96079.1	AF049352	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
SEQ ID NO: 833		
AAA34030.1	J03492	<i>Spinacia oleracea</i> glycolate oxidase (EC 1.1.3.15).
AAB40396.1	U80071	<i>Mesembryanthemum crystallinum</i> glycolate oxidase. GOX.
BAA03131.1	D14044	<i>Cucurbita sp.</i> glycolate oxidase.
AAB82143.1	AF022740	<i>Oryza sativa</i> glycolate oxidase. GOX.
CAA63482.1	X92888	<i>Lycopersicon esculentum</i> conversion of glycolate to glyoxylate + H <sub>2</sub> O <sub>2</sub> . glycolate oxidase.
AAC32392.1	AF082874	<i>Medicago sativa</i> glycolate oxidase.
AAC33509.1	U62485	<i>Nicotiana tabacum</i> photorespiration. glycolate oxidase. GLO.
AAF03097.1	AF162196	<i>Lactuca sativa</i> glycolate oxidase.
SEQ ID NO: 838		
CAA06770.1	AJ005928	<i>Brassica napus</i> squalene epoxidase homologue. Sqp1;2.
CAA06773.1	AJ005931	<i>Brassica napus</i> squalene epoxidase homologue. Sqp1;1.
BAA24448.1	AB003516	<i>Panax ginseng</i> squalene epoxidase.
CAA06223.1	AJ004923	<i>Lycopersicon esculentum</i> Squalene epoxidase. ERG.

## SEQ ID NO: 840

BAB12686.1 AP002746 *Oryza sativa*  
 putative pyrophosphate-dependent phosphofructo-1-kinase. P0671B11.1. contains ESTs  
 AU068014(C11507),C28532(C61484),AU090544(C61415).

BAA99438.1 AP002743 *Oryza sativa*  
 putative pyrophosphate-dependent phosphofructo-1-kinase. P0710E05.25. contains ESTs  
 AU068014(C11507),C28532(C61484),AU090544(C61415).

AAB88875.1 U93272 *Prunus armeniaca*  
 pyrophosphate-dependent phosphofructo-1-kinase.

CAA83683.1 Z32850 *Ricinus communis*  
 pyrophosphate-dependent phosphofructokinase beta subunit.

AAC67587.1 AF095521 *Citrus x paradisi*  
 pyrophosphate-dependent phosphofructokinase alpha subunit. PPi-PFKa.

AAA63452.1 M55191 *Solanum tuberosum*  
 pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit.

AAC67586.1 AF095520 *Citrus x paradisi*  
 pyrophosphate-dependent phosphofructokinase beta subunit. PPi-PFKb. PFP.

AAA63451.1 M55190 *Solanum tuberosum*  
 pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit.

CAA83682.1 Z32849 *Ricinus communis*  
 pyrophosphate-dependent phosphofructokinase alpha subunit.

## SEQ ID NO: 841

AAG60182.1 AC084763 *Oryza sativa*  
 putative ethylene-responsive element binding protein. OSJNBA0027P10.12.

AAK31279.1 AC079890 *Oryza sativa*  
 putative ethylene-responsive element binding protein. OSJNBB0089A17.16.

AAG43545.1 AF211527 *Nicotiana tabacum*  
 Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*  
 AP2-related transcription factor. CDBP. stress induced transcription factor.

BAA07321.1 D38123 *Nicotiana tabacum*  
 ERF1. ethylene-responsive transcription factor.

BAA97122.1 AB016264 *Nicotiana sylvestris*  
 ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

CAB93940.1 AJ238740 *Catharanthus roseus*  
 putative transcription factor. AP2-domain DNA-binding protein. orca2.

BAA87068.1 AB035270 *Matricaria chamomilla*  
 ethylene-responsive element binding protein1 homolog. McEREBP1.

BAA97124.1 AB016266 *Nicotiana sylvestris*  
 ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

CAB96900.1 AJ251250 *Catharanthus roseus*  
transcription factor. AP2-domain DNA-binding protein. orca3.

CAB96899.1 AJ251249 *Catharanthus roseus*  
transcription factor. AP2-domain DNA-binding protein. orca3.

AAC62619.1 AF057373 *Nicotiana tabacum*  
transcription factor. ethylene response element binding protein 1. EREBP1.

BAA97123.1 AB016265 *Nicotiana sylvestris*  
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.

AAC24587.1 AF071893 *Prunus armeniaca*  
AP2 domain containing protein. AP2DCP.

CAC12822.1 AJ299252 *Nicotiana tabacum*  
AP2 domain-containing transcription factor. ap2.

AAF76898.1 AF274033 *Atriplex hortensis*  
apetala2 domain-containing protein.

BAA94514.2 AP001800 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome 4, BAC clone F9D16; putative Ap2 domain protein (AL035394).

AAC14323.1 AF058827 *Nicotiana tabacum*  
TSI1. Ts1. contains putative AP2 DNA-binding domain; similar to Pt16.

AAD00708.1 U91857 *Stylosanthes hamata*  
ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

BAA76734.1 AB024575 *Nicotiana tabacum*  
ethylene responsive element binding factor.

BAB03248.1 AB037183 *Oryza sativa*  
ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.

BAB16083.1 AB036883 *Oryza sativa*  
transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.

AAF23899.1 AF193803 *Oryza sativa*  
transcription factor EREBP1. EREBP/AP2-like transcription factor.

AAF05606.1 AF190770 *Oryza sativa*  
EREBP-like protein. tsh1. TSH1; induced by ethylene.

CAB93939.1 AJ238739 *Catharanthus roseus*  
putative transcription factor. AP2-domain DNA-binding protein. orca1.

BAA78738.1 AB023482 *Oryza sativa*  
EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to *Arabidopsis thaliana* AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).

AAG43548.1 AF211530 *Nicotiana tabacum*  
Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

AAG43549.1	AF211531	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
BAA99376.1	AP002526	Oryza sativa ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
AAK31271.1	AC079890	Oryza sativa putative transcriptional factor. OSJNBb0089A17.22.
AAK01089.1	AF298231	Hordeum vulgare CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
AAG59618.1	AF239616	Hordeum vulgare CRT/DRE-binding factor. CBF.
AAC49567.1	U41466	Zea mays Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.
SEQ ID NO: 842		
AAC32034.1	AF023472	Hordeum vulgare peptide transporter. ptr1. PTR1; integral membrane protein.
BAB40113.1	AP003311	Oryza sativa putative peptide transport protein. P0024G09.4. contains ESTs D40448(S2437),C71800(E0368),AU102190(E2393), AU055921(S20154),AU102191(E2393),AU055922(S20154), C98524(E0368),AU097146(S2437).
BAB16458.1	AP002483	Oryza sativa putative peptide transport protein. P0019D06.16. contains ESTs D40448(S2437),C71800(E0368),AU102190(E2393), AU055921(S20154),AU102191(E2393),AU055922(S20154), C98524(E0368),AU097146(S2437).
AAD01600.1	AF016713	Lycopersicon esculentum LeOPT1. LeOPT1. oligopeptide transporter.
AAF07875.1	AF140606	Oryza sativa nitrate transporter. NRT1.
AAF20002.1	AF213936	Prunus dulcis amino acid/peptide transporter. PTR2. similar to transporters of nitrogenous compounds.
AAG46153.1	AC018727	Oryza sativa putative peptide transporter. OSJNBa0056G17.8.
CAC00544.1	AJ277084	Nicotiana plumbaginifolia ion transport. putative low-affinity nitrate transporter. nrt1.1.
CAC00545.1	AJ277085	Nicotiana plumbaginifolia ion transport. putative low-affinity nitrate transporter. nrt1.2.
AAA80582.1	U17987	Brassica napus putative nitrate transporter. RCH2 protein.

CAC07206.1	AJ278966	Brassica napus Low-affinity nitrate transporter. nitrate transporter. nrt1.
AAG21898.1	AC026815	Oryza sativa putative peptide transport protein. OSJNBa0079L16.13.
BAB19758.1	AB052786	Glycine max putative nitrate transporter NRT1-3. NRT1-3.
AAK15441.1	AC037426	Oryza sativa putative nitrate transporter. OSJNBb0014I11.9.
AAG21906.1	AC026815	Oryza sativa putative peptide transport protein. OSJNBa0079L16.9.
BAB19760.1	AB052788	Glycine max nitrate transporter NRT1-5. NRT1-5.
AAG46154.1	AC018727	Oryza sativa putative peptide transporter. OSJNBa0056G17.27.
BAB19757.1	AB052785	Glycine max nitrate transporter NRT1-2. NRT1-2.
BAB19756.1	AB052784	Glycine max nitrate transporter NRT1-1. NRT1-1.
BAB16322.1	AP002818	Oryza sativa putative peptide transporter-like protein. P0436E04.4.
AAB69642.1	AF000392	Lotus japonicus peptide transporter. LjNOD65.
CAA93316.1	Z69370	Cucumis sativus nitrite transporter. NiTR1.
AAD16016.1	AF080545	Nepenthes alata peptide transporter. PTR1.
BAB19759.1	AB052787	Glycine max putative nitrate transporter NRT1-4. NRT1-4.
AAD42860.1	AF154930	Prunus dulcis transporter-like protein. TLP1.

SEQ ID NO: 847

CAA61980.1	X89890	Bidens pilosa Calmodulin.
AAF73157.1	AF150059	Brassica napus calmodulin. CaM1. involved in seed germination.
BAA87825.1	AP000815	Oryza sativa ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene. Similar to O.sativa gene encoding calmodulin. (Z12828).
CAA67054.1	X98404	Capsicum annuum calmodulin-2.
AAA87347.1	M88307	Brassica juncea calmodulin.

AAA33397.1	L18912	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin. putative.
AAG27432.1	AF295637	<i>Elaeis guineensis</i> calmodulin.
CAA42423.1	X59751	<i>Daucus carota</i> calmodulin. Ccam-1.
AAG11418.1	AF292108	<i>Prunus avium</i> calmodulin.
AAA92681.1	U13882	<i>Pisum sativum</i> calcium-binding protein. calmodulin.
AAB46588.1	U83402	<i>Capsicum annuum</i> calmodulin.
AAA33706.1	M80836	<i>Petunia x hybrida</i> calmodulin. CAM81.
AAF65511.1	AF108889	<i>Capsicum annuum</i> calmodulin.
CAA43143.1	X60738	<i>Malus x domestica</i> Calmodulin. CaM.
AAA19571.1	U10150	<i>Brassica napus</i> calcium binding. calmodulin. bcm1.
CAA78301.1	Z12839	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin.
BAA88540.1	AP000969	<i>Oryza sativa</i> ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAB36130.1	S81594	<i>Vigna radiata</i> auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAC36059.1	AF042840	<i>Oryza sativa</i> calmodulin. CaM1.
AAA33901.1	L18913	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin. putative.
AAA33900.1	L18914	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.
AAA34237.1	L20691	<i>Vigna radiata</i> calmodulin.
CAA78288.1	Z12828	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.
AAA32938.1	M27303	<i>Hordeum vulgare</i> calmodulin.
CAA78287.1	Z12827	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.

AAC49587.1	U49105	Triticum aestivum calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum calmodulin TaCaM3-3. calcium-binding protein.
AAC49583.1	U48692	Triticum aestivum calmodulin TaCaM2-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum calmodulin TaCaM3-1. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum calmodulin TaCaM2-2. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum calmodulin TaCaM1-1. calcium-binding.
AAA03580.1	L01431	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAC36058.1	AF042839	Oryza sativa calmodulin. CaM2.
AAA85156.1	U20296	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34014.1	L01432	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAD10244.1	AF030032	Phaseolus vulgaris calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
CAA36644.1	X52398	Medicago sativa calmodulin (AA 1-149).
AAA85155.1	U20294	Solanum tuberosum calcium-binding protein. calmodulin.
AAB68399.1	U79736	Helianthus annuus calmodulin. HaCaM.
AAA62351.1	U20295	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34238.1	L20507	Vigna radiata calmodulin.
AAA85157.1	U20297	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34013.1	L01430	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-1. putative.

AAA33705.1 M80831 *Petunia x hybrida*  
calmodulin-related protein. CAM53.

CAA74307.1 Y13974 *Zea mays*  
calmodulin.

CAA54583.1 X77397 *Zea mays*  
calmodulin. CaM2.

SEQ ID NO: 848

CAA06486.1 AJ005340 *Linum usitatissimum*  
IAA amidohydrolase. homolog.

SEQ ID NO: 850

BAB17350.1 AP002747 *Oryza sativa*  
putative nodulin. P0698G03.34. contains ESTs  
D39891(S1543),D41717(S4395),AU033037(S1543).

BAA85440.1 AP000616 *Oryza sativa*  
ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.;  
similar to *Medicago nodulin N21*-like protein (AC004218).

CAB53493.1 AJ245900 *Oryza sativa*  
CAA303720.1 protein. q3037.20. Similar to *Medicago nodulin N21* (MtN21).

SEQ ID NO: 852

AAD16018.1 AF081514 *Taxus canadensis*  
prenyltransferase. geranylgeranyl diphosphate synthase. geranylgeranyl pyrophosphate  
synthase.

SEQ ID NO: 853

BAB32588.1 AB055807 *Momordica charantia*  
inhibitor against trypsin. bgit.

AAA34180.1 J05094 *Lycopersicon peruvianum*  
proteinase inhibitor I precursor.

AAA34198.1 M59427 *Lycopersicon peruvianum*  
proteinase inhibitor I. proteinase inhibitor I.

CAB61327.1 AJ132473 *Amaranthus hypochondriacus*  
Proteinase inhibition. trypsin inhibitor.

AAA60745.1 J04099 *Lycopersicon esculentum*  
proteinase inhibitor I. ER1.

CAA78269.1 Z12623 *Nicotiana tabacum*  
Putative precursor of serine proteinase inhibitor type I. Pre-pro-proteinase inhibitor I.

CAA47461.1 X67076 *Nicotiana tabacum*  
inhibitor of microbial serine proteinases (major isoform). TIMPa.

CAA78265.1 Z12619 *Nicotiana tabacum*  
precursor for serine proteinase inhibitor I. Pre-pro-proteinase inhibitor I.

CAA47460.1 X67075 *Nicotiana tabacum*  
inhibitor of microbial serine proteinases (minor isoform). TIMPb.

AAA34067.1 M74102 *Nicotiana sylvestris*  
pre-pro-proteinase inhibitor I.

AAC49603.1	U30861	Solanum tuberosum serine proteinase inhibitor. wound-inducible proteinase inhibitor I.
BAA02823.1	D13662	Nicotiana glauca X Nicotiana langsdorffii genetic tumor-related proteinase inhibitor I precursor. GTI.
AAA34199.1	K03290	Lycopersicon esculentum wound-induced proteinase inhibitor I prepropeptide.
AAA34200.1	M13938	Lycopersicon esculentum proteinase inhibitor I. PIIF.
AAA69780.1	L06137	Solanum tuberosum proteinase inhibitor I. pin1. putative.
AAA72133.1	L06985	Solanum tuberosum proteinase inhibitor I. pin1. The 'a' of the first atg is missing.
CAA78259.1	Z12611	Solanum tuberosum proteinase inhibitor I.
AAA69781.1	L06606	Solanum tuberosum proteinase inhibitor I. precursor.
CAA48136.1	X67950	Solanum tuberosum protease inhibitor I. pin1.
CAA47907.1	X67675	Solanum tuberosum proteinase inhibitor I. pin1.
CAB71340.1	AJ250663	Hordeum vulgare putative proteinase inhibitor. bci-7. similarity to subtilisin/chymotrypsin inhibitor.
CAA57677.1	X82187	Zea mays serine proteinase inhibitor. substilin /chymotrypsin-like inhibitor. pis7.
CAA55588.1	X78988	Zea mays proteinase inhibitor. MPI.
CAA49593.1	X69972	Zea mays proteinase inhibitor. MPI.
AAA33816.1	M17108	Solanum tuberosum proteinase inhibitor I. precursor.
CAA57307.1	X81647	Cucurbita maxima Pumpkin fruit trypsin inhibitor. pfiAF4.
CAA57203.1	X81447	Cucurbita maxima Pumpkin Fruit Chymotrypsin Inhibitor. pfiBM7.
SEQ ID NO: 859		
AAC34855.1	AF082030	Hemerocallis hybrid cultivar senescence-associated protein 5. SA5. mRNA accumulates in senescing petals and accumulation is induced by exogenous ABA.
AAG13616.1	AC078840	Oryza sativa putative senescence-associated protein. OSJNBb0073N24.21.
SEQ ID NO: 864		
AAF62403.1	AF212183	Nicotiana tabacum harpin inducing protein. hin1. similar to hin1 protein.

CAA68848.1 Y07563 Nicotiana tabacum  
activated during hypersensitive response. hin1.

AAB97367.1 AF039532 Oryza sativa  
harpin induced gene 1 homolog. Hin1.

SEQ ID NO: 871

AAC61839.1 AF025430 Papaver somniferum  
berberine bridge enzyme. bbe1. (S)-reticuline:oxygen oxidoreductase (methylene bridge forming).

AAB20352.1 S65550 Eschscholzia californica  
(S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming). /gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig 2; berberine bridge enzyme.

AAC39358.1 AF005655 Eschscholzia californica  
oxidizes the N-methyl group of (S)-reticuline to the berberine bridge carbon C-8 of (S)-scoulerine in berberine and benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1. covalently-bound FAD-dependent oxidase; elicitor-inducible.

AAD17487.1 AF049347 Berberis stolonifera  
Catalyzes the oxidative cyclization of the N-methyl group of (S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine. berberine bridge enzyme. bbe1. Covalently flavinylated oxidase of isoquinoline alkaloid biosynthesis in plants.

SEQ ID NO: 872

AAF98369.1 AF158253 Nicotiana tabacum  
patatin-like protein 3. PAT3. NtPat3.

CAA73328.1 Y12793 Cucumis sativus  
mobilization of fat during seed germination. patatin-like protein.

CAA11042.1 AJ223039 Hevea brasiliensis  
latex allergen. sequence similarity to patatins.

AAF25553.1 AF113546 Hevea brasiliensis  
latex protein allergen Hev b 7. putative PLA2; similar to Solanum tubulin patatin encoded by GenBank Accession Number X03932.

CAA11041.1 AJ223038 Hevea brasiliensis  
latex allergen. with sequence similarity to patatins.

AAC27724.1 U80598 Hevea brasiliensis  
latex patatin homolog. putative PLA2; latex protein allergen; similar to Solanum tubulin patatin encoded by GenBank Accession Number X03932.

AAK27797.1 AF318315 Vigna unguiculata  
patatin-like protein.

AAK18751.1 AF193067 Vigna unguiculata  
patatin-like protein.

AAB08428.1 U68484 Nicotiana tabacum  
patatin homolog.

AAD22170.1 AF061282 Sorghum bicolor  
patatin-like protein.

WO 03/000898

AAF98368.1 AF158027 Nicotiana tabacum  
patatin-like protein 1. PAT1. NtPat1.

AAD22169.1 AF061282 Sorghum bicolor  
patatin-like protein.

CAA81735.1 Z27221 Solanum tuberosum  
patatin.

CAA31575.1 X13178 Solanum tuberosum  
patatin B2 (AA 1 - 386).

AAA33819.1 M18880 Solanum tuberosum  
patatin.

CAA31576.1 X13179 Solanum tuberosum  
patatin B1 (377 AA) (1 is 3rd base in codon).

CAA27588.1 X03956 Solanum tuberosum  
patatin.

AAA33828.1 M21879 Solanum tuberosum  
patatin.

CAA27571.1 X03932 Solanum tuberosum  
patatin.

CAA25592.1 X01125 Solanum tuberosum  
patatin.

AAA66198.1 U09331 Solanum brevidens  
patatin precursor.

AAB08427.1 U68483 Nicotiana tabacum  
patatin homolog.

AAF98370.1 AF158254 Nicotiana tabacum  
patatin-like protein 2. PAT2.

AAD22149.1 AF061282 Sorghum bicolor  
patatin-like protein. similar to the EST sequences E0496(panicle at flowering stage), R2382  
(root), R2382 (root), S4036 (shoot), S3728 (shoot), S13457 (green shoot).

SEQ ID NO: 875

BAA93022.1 AP001552 Oryza sativa  
ESTs C74776(E51022),C26123(C116681) correspond to a region of the predicted gene.  
Similar to Arabidopsis thaliana cultivar Landsberg extra-large G-protein (AF060942).

SEQ ID NO: 876

BAA87853.1 AP000816 Oryza sativa  
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative  
NAK-like Ser/Thr protein kinase. (AF001308).

AAK21965.1 AY028699 Brassica napus  
receptor protein kinase PERK1.

AAD21872.1 AF078082 Phaseolus vulgaris  
receptor-like protein kinase homolog RK20-1.

AAK00425.1 AC069324 Oryza sativa  
Putative protein kinase. OSJNBa0071K19.11.

BAB39873.1 AP002882 *Oryza sativa*  
putative protein kinase. P0439B06.8. contains ESTs  
AU056701(S20808),AU056702(S20808).

AAA33915.1 L27821 *Oryza sativa*  
receptor type serine/threonine kinase. protein kinase.

BAA82556.1 AB030083 *Populus nigra*  
lectin-like protein kinase. PnLPK.

AAK11674.1 AF339747 *Lophopyrum elongatum*  
protein kinase. ESI47.

AAF43496.1 AF131222 *Lophopyrum elongatum*  
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and  
ABA treatment.

AAG59657.1 AC084319 *Oryza sativa*  
putative protein kinase. OSJNBa0004B24.20.

AAG03090.1 AC073405 *Oryza sativa*  
Similar to an *Arabidopsis* somatic embryogenesis receptor-like kinase (AC007504).

AAB93834.1 U82481 *Zea mays*  
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein  
kinase.

AAF66615.1 AF142596 *Nicotiana tabacum*  
LRR receptor-like protein kinase.

AAG25966.1 AF302082 *Nicotiana tabacum*  
cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly  
after cytokinin treatment.

AAB09771.1 U67422 *Zea mays*  
CRINKLY4 precursor. cr4. receptor kinase homolog.

AAF34428.1 AF172282 *Oryza sativa*  
receptor-like protein kinase. DUPR11.18.

BAB07906.1 AP002835 *Oryza sativa*  
putative S-receptor kinase. P0417G05.14.

AAC23542.1 U20948 *Ipomoea trifida*  
receptor protein kinase. IRK1.

BAA94516.1 AP001800 *Oryza sativa*  
Similar to *Zea mays* S-domain receptor-like protein kinase (AJ010166).

BAA87852.1 AP000816 *Oryza sativa*  
Similar to putative Ser/Thr protein kinase. (AC004218).

BAA92221.1 AP001278 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome II BAC F12L6 genomic sequence, putative  
protein kinase. (AC004218).

CAA73134.1 Y12531 *Brassica oleracea*  
serine/threonine kinase. BRLK.

BAA92954.1 AP001551 *Oryza sativa*  
Similar to *Oryza sativa* protein kinase (OSPK10) mRNA. (L27821).

AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
CAB51834.1	00069	Oryza sativa I1332.5. contains eukaryotic protein kinase domain PF.
BAA06538.1	D31737	Nicotiana tabacum protein-serine/threonine kinase.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
CAB89179.1	AJ245479	Brassica napus subsp. napus ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus serine/threonine kinase receptor.
BAA92837.1	AB032474	Brassica oleracea S60 S-locus receptor kinase. SRK60.
AAA33000.1	M76647	Brassica oleracea receptor protein kinase. SKR6.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
BAB07904.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.12.
BAA94518.1	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAA07577.2	D38564	Brassica rapa receptor protein kinase SRK12.
CAA74662.1	Y14286	Brassica oleracea SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAA07576.1	D38563	Brassica rapa receptor protein kinase SRK8.
BAB07999.1	AP002525	Oryza sativa putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB07905.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.13.

BAB03429.1	AP002817	Oryza sativa
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).		
		SEQ ID NO: 883
BAA90510.2 AP001111 Oryza sativa rice EST AU030811, similar to rice Ca <sup>2+</sup> -ATPase (U82966).		
AAF73985.1	AF096871	Zea mays
calcium pump. calcium ATPase. cap1.		
CAA63790.1	X93592	Dunaliella bioculata
P-type ATPase. ca1. calcium pumping; CA1.		
AAD11618.1	AF050496	Lycopersicon esculentum
Ca <sup>2+</sup> -ATPase. LCA1B; alternative transcript.		
AAA34138.1	M96324	Lycopersicon esculentum
The calcium ATPase is a calcium ion pump. Ca <sup>2+</sup> -ATPase. LCA1.		
AAB58910.1	U82966	Oryza sativa
Ca <sup>2+</sup> -ATPase.		
AAD11617.1	AF050495	Lycopersicon esculentum
Ca <sup>2+</sup> -ATPase. LCA1A; alternative transcript.		
AAG28435.1	AF195028	Glycine max
plasma membrane Ca <sup>2+</sup> -ATPase. SCA1.		
AAG28436.1	AF195029	Glycine max
plasma membrane Ca <sup>2+</sup> -ATPase. SCA2.		
CAA68234.1	X99972	Brassica oleracea
calmodulin-stimulated calcium-ATPase.		
AAD31896.1	AF145478	Mesembryanthemum crystallinum
calcium ATPase.		
AAB60276.1	U09989	Zea mays
H(+)-transporting ATPase. Mhal.		
CAB69824.1	AJ271439	Prunus persica
plasma membrane H <sup>+</sup> ATPase. PPA1.		
AAD46187.1	AF156683	Nicotiana plumbaginifolia
plasma membrane proton ATPase. pma8.		
BAA01058.1	D10207	Oryza sativa
H-ATPase. OSA1.		
AAB49042.1	U54690	Dunaliella acidophila
plasma membrane proton ATPase. dha1. DaDHA1; proton pump.		
AAA34173.1	M60166	Lycopersicon esculentum
H <sup>+</sup> -ATPase. LHA1.		
CAA52107.1	X73901	Dunaliella bioculata
plasma membrane ATPase. pma1.		

AAB35314.2 S79323 *Vicia faba*  
plasma membrane H(+)-ATPase precursor. plasma membrane H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.

BAA06629.1 D31843 *Oryza sativa*  
plasma membrane H+-ATPase. OSA2.

AAA34094.1 M80489 *Nicotiana plumbaginifolia*  
plasma membrane H+ ATPase. pma1.

BAA08134.1 D45189 *Zostera marina*  
plasma membrane H+-ATPase. zha1.

CAB85494.1 AJ132891 *Medicago truncatula*  
proton pump. H+-ATPase. ha1.

CAB85495.1 AJ132892 *Medicago truncatula*  
proton pump. H+-ATPase. ha1.

AAB84202.2 AF029256 *Kosteletzky virginica*  
plasma membrane proton ATPase. ATP1.

CAA47275.1 X66737 *Nicotiana plumbaginifolia*  
plasma membrane H+-ATPase. pma4.

CAA54045.1 X76535 *Solanum tuberosum*  
H(+)-transporting ATPase. PHA2.

AAD46186.1 AF156679 *Nicotiana plumbaginifolia*  
plasma membrane proton ATPase. pma6.

AAB17186.1 U72148 *Lycopersicon esculentum*  
plasma membrane H+-ATPase. LHA4. plasma membrane proton pumping ATPase.

CAB69823.1 AJ271438 *Prunus persica*  
plasma membrane H+ ATPase. PPA2.

AAB41898.1 U84891 *Mesembryanthemum crystallinum*  
plasma membrane proton pump. H+-transporting ATPase. PMA.

CAC29436.1 AJ310524 *Vicia faba*  
P-type H+-ATPase. ha5. predominantly expressed in guard cells and flowers.

BAA37150.1 AB022442 *Vicia faba*  
p-type H+-ATPase. VHA2.

CAA59800.1 X85805 *Zea mays*  
H(+)-transporting ATPase. MHA-2.

CAA59799.1 X85804 *Phaseolus vulgaris*  
H(+)-transporting ATPase. BHA-1.

CAC29435.1 AJ310523 *Vicia faba*  
P-type H+-ATPase. vha4. predominantly expressed in flowers.

AAD46188.1 AF156691 *Nicotiana plumbaginifolia*  
plasma membrane proton ATPase. pma9.

AAA34099.1 M80491 *Nicotiana plumbaginifolia*  
plasma membrane H+ ATPase. pma3.

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AAA34052.1 M27888 *Nicotiana plumbaginifolia*  
H<sup>+</sup>-translocating ATPase.

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CAA54046.1 X76536 *Solanum tuberosum*  
H(+) -transporting ATPase. PHA1.

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AAA34098.1 M80490 *Nicotiana plumbaginifolia*  
plasma membrane H<sup>+</sup> ATPase. pma3.

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AAD55399.1 AF179442 *Lycopersicon esculentum*  
plasma membrane H<sup>+</sup>-ATPase isoform LHA2. LHA2.

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AAF98344.1 AF275745 *Lycopersicon esculentum*  
plasma membrane H<sup>+</sup>-ATPase. LHA2. P-type ion pump.

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AAG01028.1 AF289025 *Cucumis sativus*  
plasma membrane H<sup>+</sup>-ATPase.

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AAK31799.1 AY029190 *Lilium longiflorum*  
plasma membrane H<sup>+</sup> ATPase. LILHA1.

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AAA81348.1 U38965 *Vicia faba*  
p-type H<sup>+</sup>-ATPase. VHA2.

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AAK32119.1 AF308817 *Hordeum vulgare*  
plasmalemma H<sup>+</sup>-ATPase 2.

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AAK32118.1 AF308816 *Hordeum vulgare*  
plasmalemma H<sup>+</sup>-ATPase 1.

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AAA20600.1 U08984 *Zea mays*  
plasma-membrane H<sup>+</sup> ATPase. Zmpma1.

SEQ ID NO: 884

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AAD21872.1 AF078082 *Phaseolus vulgaris*  
receptor-like protein kinase homolog RK20-1.

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AAB93834.1 U82481 *Zea mays*  
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

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CAA73134.1 Y12531 *Brassica oleracea*  
serine/threonine kinase. BRLK.

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AAC23542.1 U20948 *Ipomoea trifida*  
receptor protein kinase. IRK1.

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CAA67145.1 X98520 *Brassica oleracea*  
receptor-like kinase. SFR2.

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CAA73133.1 Y12530 *Brassica oleracea*  
serine /threonine kinase. ARLK.

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BAA23676.1 AB000970 *Brassica rapa*  
receptor kinase 1. BcRK1.

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CAB41879.1 Y18260 *Brassica oleracea*  
SRK15 protein. SRK15. receptor-like kinase.

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CAB41878.1 Y18259 *Brassica oleracea*  
SRK5 protein. SRK5. receptor-like kinase.

CAA74662.1	Y14286	Brassica oleracea
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.		
CAA74661.1	Y14285	Brassica oleracea
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.		
BAA06285.1	D30049	Brassica rapa
S-receptor kinase SRK9.		
BAA21132.1	D88193	Brassica rapa
S-receptor kinase. SRK9 (B.c).		
BAA92836.1	AB032473	Brassica oleracea
S18 S-locus receptor kinase. SRK18.		
CAA79355.1	Z18921	Brassica oleracea
S-receptor kinase-like protein.		
AAA33000.1	M76647	Brassica oleracea
receptor protein kinase. SKR6.		
AAA62232.1	U00443	Brassica napus
S-receptor kinase. protein contains an immunoglobulin-like domain.		
AAA33008.1	M97667	Brassica napus
serine/threonine kinase receptor.		
CAB89179.1	AJ245479	Brassica napus subsp. napus
ser /thr kinase. S-locus receptor kinase. srk.		
BAB18292.1	AP002860	Oryza sativa
putative receptor-like protein kinase. P0409B08.19.		
AAD52097.1	AF088885	Nicotiana tabacum
receptor-like kinase CHRK1. Chrk1.		
BAA92837.1	AB032474	Brassica oleracea
S60 S-locus receptor kinase. SRK60.		
BAB21001.1	AB054061	Brassica rapa
S locus receptor kinase. SRK22.		
BAA07576.1	D38563	Brassica rapa
receptor protein kinase SRK8.		
BAA07577.2	D38564	Brassica rapa
receptor protein kinase SRK12.		
AAK02023.1	AC074283	Oryza sativa
Putative protein kinase-like. OSJNBA0087H07.5.		
CAA79324.1	Z18884	Brassica oleracea
S-receptor kinase related protein.		
BAB16871.1	AP002537	Oryza sativa
putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).		

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BAB39873.1 AP002882 *Oryza sativa*  
 putative protein kinase. P0439B06.8. contains ESTs  
 AU056701(S20808),AU056702(S20808).

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AAK21965.1 AY028699 *Brassica napus*  
 receptor protein kinase PERK1.

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BAA87853.1 AP000816 *Oryza sativa*  
 EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative  
 NAK-like Ser/Thr protein kinase. (AF001308).

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CAB51836.1 AJ243961 *Oryza sativa*  
 Putitive Ser/Thr protein kinase. 11332.7.

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AAA33915.1 L27821 *Oryza sativa*  
 receptor type serine/threonine kinase. protein kinase.

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BAB21240.1 AP002953 *Oryza sativa*  
 Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

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AAK00425.1 AC069324 *Oryza sativa*  
 Putative protein kinase. OSJNBa0071K19.11.

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BAA92954.1 AP001551 *Oryza sativa*  
 Similar to *Oryza sativa* protein kinase (OSPK10) mRNA. (L27821).

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AAF66615.1 AF142596 *Nicotiana tabacum*  
 LRR receptor-like protein kinase.

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BAB17139.1 AP002867 *Oryza sativa*  
 putative receptor kinase. P0463F06.31.

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SEQ ID NO: 885

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CAA80358.1 Z22645 *Solanum tuberosum*  
 cleavage of sucrose to glucose and fructose. beta-fructofuranosidase.

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CAA79676.1 Z21486 *Solanum tuberosum*  
 cleavage of sucrose to glucose and fructose. beta-fructofuranosidase.

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CAA57428.1 X81834 *Nicotiana tabacum*  
 beta-fructofuranosidase. Ntbfruc1. beta-fructosidase.

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CAA49162.1 X69321 *Daucus carota*  
 beta-fructofuranosidase. Inva1\*DC1.

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CAA57389.1 X81792 *Chenopodium rubrum*  
 beta-fructofuranosidase. CIN1.

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AAC17166.1 AF063246 *Pisum sativum*  
 hydrolyzes sucrose to glucose and fructose. cell wall invertase. bfruct1. isoform Pcl-2; the  
 Pcl-1 isoform is in the file with GenBank Accession Number X85327; beta-  
 fructofuranosidase.

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CAA59677.1 X85327 *Pisum sativum*  
 hydprlyze sucrose into fructose and glucose. invertase. bfruct1. beta-fructofuranosidase.

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AAD02263.1 AF043346 *Zea mays*  
 sucrose hydrolysis. cell wall invertase. incw3. Incw3; beta-fructofuranosidase.

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CAA84526.1 Z35162 *Vicia faba*  
 hydrolyze sucrose. beta-fructofuranosidase; cell wall invertase I; fructosidase. VFCWINV1.

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AAC96065.1	AF030420	Triticum aestivum hydrolyzes sucrose. cell wall invertase. IVR1. hydrolase; beta-fructofuranosidase; fructosidase.
CAA53099.1	X75353	Daucus carota beta-fructofuranosidase.
AAB68679.1	U92438	Phaseolus vulgaris soluble acid invertase. PVSA1; potential vacuolar targeted enzyme; beta-fructofuranosidase.
CAA89992.1	Z49831	Vicia faba hydrolyze sucrose. vacuolar invertase; beta-fructofuranosidase. VFVCINV.
CAA53097.1	X75351	Daucus carota beta-fructofuranosidase.
CAA77267.1	Y18707	Daucus carota beta-fructofuranosidase, isoform I. Inv*Dc4. soluble acid invertase.
CAA53098.1	X75352	Daucus carota beta-fructofuranosidase.
CAA77266.1	Y18706	Daucus carota beta-fructofuranosidase, isoform II. Inv*Dc5. soluble acid invertase.
AAC96066.1	AF030421	Triticum aestivum hydrolyzes sucrose. cell wall invertase. IVR3. hydrolase; beta-fructofuranosidase; fructosidase.
AAG36943.1	AF274299	Brassica oleracea cleaves sucrose into glucose and fructose at acid pH optima. acid invertase AI7-3. sucrose hydrolysing enzyme; beta-fructofuranosidase.
SEQ ID NO: 887		
AAD10836.1	U52079	Solanum tuberosum P-glycoprotein. pmdr1. binds ATP; ATPase; transporter; transmembrane protein.
BAA96612.1	AP002482	Oryza sativa Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411).
AAG49002.1	AY013246	Hordeum vulgare putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.
AAG45492.1	AY013245	Oryza sativa 36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.
BAA83352.1	AP000391	Oryza sativa ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
AAG49003.1	AY013246	Hordeum vulgare putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
BAB17113.1	AP002866	Oryza sativa putative white protein; ATP-binding cassette transporter. P0410E01.34.

BAA90508.1	AP001111	Oryza sativa similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA90507.1	AP001111	Oryza sativa similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAB16495.1	AP002861	Oryza sativa putative ABC transporter ATP-binding protein. P0665D10.21.
BAB21276.1	AP002844	Oryza sativa putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
BAB21275.1	AP002844	Oryza sativa putative ABC transporter protein. P0410E03.6.
BAB21273.1	AP002844	Oryza sativa putative ABC transporter protein. P0410E03.4.
BAB40032.1	AP003046	Oryza sativa putative ABC transporter. P0445D12.3.
SEQ ID NO: 888		
AAD21872.1	AF078082	Phaseolus vulgaris receptor-like protein kinase homolog RK20-1.
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
AAA33000.1	M76647	Brassica oleracea receptor protein kinase. SKR6.
CAB89179.1	AJ245479	Brassica napus subsp. napus ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus serine/threonine kinase receptor.
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
BAA92836.1	AB032473	Brassica oleracea S18 S-locus receptor kinase. SRK18.

CAA74662.1	Y14286	Brassica oleracea
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.		
CAA79355.1	Z18921	Brassica oleracea
S-receptor kinase-like protein.		
CAB41879.1	Y18260	Brassica oleracea
SRK15 protein. SRK15. receptor-like kinase.		
BAA06285.1	D30049	Brassica rapa
S-receptor kinase SRK9.		
BAA21132.1	D88193	Brassica rapa
S-receptor kinase. SRK9 (B.c).		
CAB41878.1	Y18259	Brassica oleracea
SRK5 protein. SRK5. receptor-like kinase.		
BAA92837.1	AB032474	Brassica oleracea
S60 S-locus receptor kinase. SRK60.		
BAA07577.2	D38564	Brassica rapa
receptor protein kinase SRK12.		
BAB21001.1	AB054061	Brassica rapa
S locus receptor kinase. SRK22.		
BAA07576.1	D38563	Brassica rapa
receptor protein kinase SRK8.		
AAD52097.1	AF088885	Nicotiana tabacum
receptor-like kinase CHRK1. Chrk1.		
AAK02023.1	AC074283	Oryza sativa
Putative protein kinase-like. OSJNBa0087H07.5.		
BAB18292.1	AP002860	Oryza sativa
putative receptor-like protein kinase. P0409B08.19.		
BAA87853.1	AP000816	Oryza sativa
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).		
AAK21965.1	AY028699	Brassica napus
receptor protein kinase PERK1.		
BAB21240.1	AP002953	Oryza sativa
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).		
BAB39873.1	AP002882	Oryza sativa
putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).		
BAB17331.1	AP002747	Oryza sativa
putative receptor kinase. P0698G03.12.		
BAB17139.1	AP002867	Oryza sativa
putative receptor kinase. P0463F06.31.		
AAK00425.1	AC069324	Oryza sativa
Putative protein kinase. OSJNBa0071K19.11.		

BAB16871.1 AP002537 Oryza sativa  
putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs  
C22608(R3192),D25110(R3192).

BAA92954.1 AP001551 Oryza sativa  
Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).

CAB51836.1 AJ243961 Oryza sativa  
Putitive Ser/Thr protein kinase. I1332.7.

AAF78016.1 AF238472 Oryza sativa  
receptor-like kinase. RLG15. protein kinase.

BAB39451.1 AP003338 Oryza sativa  
putative receptor kinase. OJ1212\_B09.24.

SEQ ID NO: 890

AAB47181.1 S82324 Zea mays  
/gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.

BAA22410.1 D38452 Zea mays  
calcium-dependent protein kinase-related kinase.

BAA12692.1 D84508 Zea mays  
CDPK-related protein kinase. Does not require calcium for its activity.

AAG01179.1 AF289237 Zea mays  
calcium/calmodulin dependent protein kinase MCK2. MCK2.

CAA58750.1 X83869 Daucus carota  
CDPK-related protein kinase. CRK (or PK421).

BAA12691.1 D84507 Zea mays  
CDPK-related protein kinase. Does not require calcium for its activity (by similarity).

AAC24961.1 AF009337 Tradescantia virginiana  
CDPK-related protein kinase. CRK1.

AAF23901.2 AF194414 Oryza sativa  
calcium-dependent protein kinase. CDPK5. OsCDPK5.

AAF23900.1 AF194413 Oryza sativa  
calcium-dependent protein kinase. CDPK1. OsCDPK1.

AAC78558.1 AF030879 Solanum tuberosum  
protein kinase CPK1.

AAD17800.1 AF090835 Mesembryanthemum crystallinum  
Ca<sup>2+</sup>-dependent protein kinase: CPK1. serine/threonine protein kinase.

AAB49984.1 U90262 Cucurbita pepo  
calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine protein kinase that is activated by direct binding of calcium.

CAA07481.1 AJ007366 Zea mays  
calcium-dependent protein kinase.

BAB21081.1 AP002819 Oryza sativa  
putative calcium-dependent protein kinase. P0501G01.10.

BAA12715.1 D85039 Zea mays  
calcium-dependent protein kinase.

AAC25423.1	AF072908	Nicotiana tabacum calcium-dependent protein kinase. CDPK1.
CAA39936.1	X56599	Daucus carota calcium- dependent protein kinase. DcPK431.
CAA57157.1	X81394	Oryza sativa calcium-dependent protein kinase. OSCPK2.
AAF21062.1	AF216527	Dunaliella tertiolecta calcium-dependent protein kinase. CPK1; CDPK.
BAA81751.1	AB017517	Marchantia polymorpha calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
BAA81749.1	AB017515	Marchantia polymorpha calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
AAB88537.1	AF035944	Fragaria x ananassa calcium-dependent protein kinase. MAX17.
BAA81750.1	AB017516	Marchantia polymorpha calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
BAA81748.1	AB017515	Marchantia polymorpha calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
AAA69507.1	U28376	Zea mays calcium-dependent protein kinase. MZECDPK2.
AAA61682.1	L27484	Zea mays calcium-dependent protein kinase. CDPK.
AAB80693.1	U69174	Glycine max calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.
BAA13232.1	D87042	Zea mays Calcium-dependent protein kinase.
BAA13440.1	D87707	Ipomoea batatas calcium dependent protein kinase. CDPK.
CAA89202.1	Z49233	Chlamydomonas eugametos calcium-stimulated protein kinase.
AAB70706.1	U82087	Tortula ruralis calmodulin-like domain protein kinase. TrCPK1.
AAD28192.2	AF115406	Solanum tuberosum calcium-dependent protein kinase. CDPK; catalytic domain.
AAC49405.1	U08140	Vigna radiata calcium dependent protein kinase. CDPK.
BAA12338.1	D84408	Zea mays calcium dependent protein kinase. ZmCDPK1.
CAA65500.1	X96723	Medicago sativa protein kinase. CDPK.

BAA85396.1	AP000615	Oryza sativa ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844) correspond to a region of the predicted gene.; similar to calcium dependent protein kinase. (AF048691).
AAA33443.1	L15390	Zea mays calcium-dependent protein kinase. CDPK.
AAB80692.1	U69173	Glycine max calmodulin-like domain protein kinase isoenzyme beta. CDPK beta.
CAA57156.1	X81393	Oryza sativa calcium-dependent protein kinase. OSCPKII.
AAC05270.1	AF048691	Oryza sativa calcium dependent protein kinase. CDPK12.
AAK26164.1	AY027885	Cucumis sativus calcium-dependent calmodulin-independent protein kinase 5. CDPK5. CsCDPK5.
AAG46110.1	AC073166	Oryza sativa calcium-dependent protein kinase. OSJNBb0064P21.2.
BAA02698.1	D13436	Oryza sativa calcium-dependent protein kinase. spk.
BAA90814.1	AP001168	Oryza sativa ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
AAF19401.1	AF203479	Glycine max phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.
CAB46228.1	Y18055	Arachis hypogaea calcium dependent protein kinase. CDPK.
AAF19403.1	AF203481	Lycopersicon esculentum phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.
AAF19402.1	AF203480	Lycopersicon esculentum phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.
SEQ ID NO: 892		
AAF20931.1	AF206721	Brassica juncea ascorbate oxidase.
BAA07734.1	D43624	Nicotiana tabacum ascorbate oxidase precursor.
AAA33119.1	J04494	Cucumis sativus ascorbate oxidase precursor (EC 1.10.3.3).
CAA75577.1	Y15295	Medicago truncatula L-ascorbate oxidase. MtN23.
AAF35911.2	AF233594	Cucumis melo ascorbate oxidase AO4. multicopper oxidase.

CAA39300.1	X55779	Cucurbita sp. ascorbate oxidase.
BAA09528.1	D55677	Cucurbita maxima ascorbate oxidase. AAO.
AAF35910.1	AF233593	Cucumis melo ascorbate oxidase AO1. multicopper oxidase.
CAA71275.1	Y10226	Cucumis melo L-ascorbate oxidase. ao3.
AAF20932.1	AF206722	Brassica juncea ascorbate oxidase.
AAF20933.1	AF206723	Brassica juncea ascorbate oxidase.
CAA71273.1	Y10224	Cucumis melo L-ascorbate oxidase. ao1.
CAA71274.1	Y10225	Cucumis melo L-ascorbate oxidase. ao1.
BAA20520.1	AB004799	Oryza sativa ascorbate oxidase.
AAF33751.1	AF202460	Capsicum annuum ascorbic acid oxidase.
AAB17193.1	U73105	Liriodendron tulipifera monolignol polymerization; lignin biosynthesis. laccase. LAC2-3. diphenol oxidase; blue copper oxidase.
AAB17191.1	U73103	Liriodendron tulipifera monolignol polymerization; lignin biosynthesis. laccase. LAC2-1. diphenol oxidase; blue copper oxidase.
AAC49536.1	U43542	Nicotiana tabacum diphenol oxidase. laccase.
AAB17194.1	U73106	Liriodendron tulipifera monolignol polymerization; lignin biosynthesis. laccase. LAC2-4. diphenol oxidase; blue copper oxidase.
AAB17192.1	U73104	Liriodendron tulipifera monolignol polymerization; lignin biosynthesis. laccase. LAC2-2. diphenol oxidase; blue copper oxidase.
AAC04576.1	AF047697	Oryza sativa p-diphenol oxidase. putative high-pI laccase.
AAB09228.1	U12757	Acer pseudoplatanus monolignol polymerization; lignin biosynthesis. laccase. diphenol oxidase.
CAA45554.1	X64257	Brassica napus Bp10. protein homologous to ascorbate oxidase.
AAC49538.1	U45243	Nicotiana tabacum diphenol oxidase. laccase.

AAC49537.1	U43543	Nicotiana tabacum diphenol oxidase. laccase.
AAD02557.1	AF049931	Petunia x hybrida PGPS/NH15. PGPS/NH15. ascorbate oxidase homolog.
SEQ ID NO: 894		
CAB43505.1	AJ239051	Cicer arietinum cytochrome P450. cyp81E2.
BAA74465.1	AB022732	Glycyrrhiza echinata cytochrome P450. CYP Ge-31.
BAA93634.1	AB025016	Lotus japonicus cytochrome P450.
BAA22422.1	AB001379	Glycyrrhiza echinata cytochrome P450. CYP81E1.
CAA04117.1	AJ000478	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-race).
CAB41490.1	AJ238439	Cicer arietinum cytochrome P450 monooxygenase. cyp81E3v2.
CAA04116.1	AJ000477	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
CAA10067.1	AJ012581	Cicer arietinum cytochrome P450. cyp81E3.
AAK38079.1	AF321855	Lolium rigidum putative cytochrome P450.
AAK38080.1	AF321856	Lolium rigidum putative cytochrome P450.
AAK38081.1	AF321857	Lolium rigidum putative cytochrome P450.
AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAC34853.1	AF082028	Hemerocallis hybrid cultivar putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3. mRNA accumulates in senescing petals.
AAG09208.1	AF175278	Pisum sativum wound-inducible P450 hydroxylase. CYP82A1.
BAA12159.1	D83968	Glycine max Cytochrome P-450 (CYP93A1).
CAA71515.1	Y10491	Glycine max putative cytochrome P450.
CAA71876.1	Y10982	Glycine max putative cytochrome P450.
CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.

AAC49188.2	U29333	Pisum sativum cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
CAA71516.1	Y10492	Glycine max putative cytochrome P450.
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
AAC39454.1	AF014802	Eschscholzia californica (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of Pisum sativum GenBank Accession Number U29333.
AAB94590.1	AF022461	Glycine max CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
CAA71877.1	Y10983	Glycine max putative cytochrome P450.
BAA84072.1	AB028152	Torenia hybrida flavone synthase II. cytochrome P450. TFNS5.
BAA13076.1	D86351	Glycine max cytochrome P-450 (CYP93A2).
AAG34695.1	AF313492	Matthiola incana putative cytochrome P450.
BAA84071.1	AB028151	Antirrhinum majus flavone synthase II. cytochrome P450. AFNS2.
AAC32274.1	AF081575	Petunia x hybrida flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.
BAA35080.1	AB015762	Nicotiana tabacum putative cytochrome P450. CYP82E1.
CAA50155.1	X70824	Solanum melongena flavonoid hydroxylase (P450). CYP75.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
BAA92894.1	AB006790	Petunia x hybrida cytochrome P450. IMT-2.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
AAB94587.1	AF022458	Glycine max CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

SEQ ID NO: 895

BAA78764.1 AB023482 *Oryza sativa*  
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAF43496.1 AF131222 *Lophopyrum elongatum*  
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.

AAK11674.1 AF339747 *Lophopyrum elongatum*  
protein kinase. ESI47.

AAG16628.1 AY007545 *Brassica napus*  
protein serine/threonine kinase BNK1.

BAA94510.1 AB041504 *Populus nigra*  
protein kinase 2. PnPK2.

BAA94509.1 AB041503 *Populus nigra*  
protein kinase 1. PnPK1.

BAA87853.1 AP000816 *Oryza sativa*  
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

BAB07999.1 AP002525 *Oryza sativa*  
putative protein kinase. P0462H08.22. contains EST C22619(S11214).

BAB03429.1 AP002817 *Oryza sativa*  
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

BAB16871.1 AP002537 *Oryza sativa*  
putative protein kinase APK1A*Arabidopsis thaliana*. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

BAB39873.1 AP002882 *Oryza sativa*  
putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

BAB39409.1 AP002901 *Oryza sativa*  
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

AAK00425.1 AC069324 *Oryza sativa*  
Putative protein kinase. OSJNBa0071K19.11.

BAB21240.1 AP002953 *Oryza sativa*  
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

AAK21965.1 AY028699 *Brassica napus*  
receptor protein kinase PERK1.

AAG59657.1 AC084319 *Oryza sativa*  
putative protein kinase. OSJNBa0004B24.20.

AAG03090.1 AC073405 *Oryza sativa*  
Similar to an *Arabidopsis* somatic embryogenesis receptor-like kinase (AC007504).

CAB51834.1 00069 *Oryza sativa*  
l1332.5. contains eukaryotic protein kinase domain PF.

AAC61805.1 U28007 *Lycopersicon esculentum*  
serine/threonine protein kinase. Pto kinase interactor 1. Pt1. Pt1 kinase.

AAF91336.1 AF249317 *Glycine max*  
Pt1 kinase-like protein. Pt1a. protein kinase.

AAF91337.1 AF249318 *Glycine max*  
Pt1 kinase-like protein. Pt1b. protein kinase.

BAB21241.1 AP002953 *Oryza sativa*  
Putative Pto kinase interactor 1. P0426D06.21. contains ESTs  
AU108280(E0721),D48017(S13927).

AAB09771.1 U67422 *Zea mays*  
CRINKLY4 precursor. cr4. receptor kinase homolog.

CAA97692.1 Z73295 *Catharanthus roseus*  
receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser.  
Mechanism: autophosphorylation in cis.

BAA92221.1 AP001278 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome II BAC F12L6 genomic sequence, putative  
protein kinase. (AC004218).

BAA87852.1 AP000816 *Oryza sativa*  
Similar to putative Ser/Thr protein kinase. (AC004218).

AAB61708.1 U93048 *Daucus carota*  
somatic embryogenesis receptor-like kinase. SERK.

AAG25966.1 AF302082 *Nicotiana tabacum*  
cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly  
after cytokinin treatment.

BAA90808.1 AP001168 *Oryza sativa*  
Similar to putative receptor-like protein kinase (AL035679).

AAF76313.1 AF220603 *Lycopersicon esculentum*  
Pto kinase. LescPth5.

AAB47421.1 U59316 *Lycopersicon esculentum*  
serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in  
tomato.

AAC23542.1 U20948 *Ipomoea trifida*  
receptor protein kinase. IRK1.

BAB19337.1 AP003044 *Oryza sativa*  
putative protein kinase. P0038C05.10. contains ESTs  
AU056335(S20481),AU056336(S20481).

AAC27894.1 AF023164 *Zea mays*  
leucine-rich repeat transmembrane protein kinase 1. ltk1.

AAF66615.1 AF142596 *Nicotiana tabacum*  
LRR receptor-like protein kinase.

CAB51480.1 Y14600 *Sorghum bicolor*  
putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA92953.1	AP001551	Oryza sativa Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).
AAK11566.1	AF318490	Lycopersicon hirsutum Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAK11567.1	AF318491	Lycopersicon hirsutum Pto-like protein kinase F. LhirPtoF.
BAA82556.1	AB030083	Populus nigra lectin-like protein kinase. PnLPK.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
SEQ ID NO: 899		
AAF61647.1	AF190634	Nicotiana tabacum UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA89009.1	AB027455	Petunia x hybrida anthocyanin 5-O-glucosyltransferase. PH1.
AAA59054.1	L34847	Zea mays conjugation of the growth hormone indole-3-acetic acid (IAA). IAA-glu synthetase. iaglu.
BAA93039.1	AB033758	Citrus unshiu limonoid UDP-glucosyltransferase. LGTase.
BAA36423.1	AB013598	Verbena x hybrida UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA36421.1	AB013596	Perilla frutescens UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.
AAF98390.1	AF287143	Brassica napus catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAA36422.1	AB013597	Perilla frutescens UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.
BAB07962.1	AP002524	Oryza sativa putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
AAK16175.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.15.
AAK16181.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.16.
AAK16178.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.5.
AAG25643.1	AF303396	Phaseolus vulgaris UDP-glucosyltransferase HRA25. putative; defense associated.

AAK16172.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.14.
BAA83484.1	AB031274	Scutellaria baicalensis UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAB36652.1	U32643	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
AAD21086.1	AF127218	Forsythia x intermedia adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAB36653.1	U32644	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS5a.
BAA12737.1	D85186	Gentiana triflora UDP-glucose:flavonoid-3-glucosyltransferase.
AAK28303.1	AF346431	Nicotiana tabacum phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAF17077.1	AF199453	Sorghum bicolor UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16180.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.21.
CAA59450.1	X85138	Lycopersicon esculentum twi1. homologous to glucosyltransferases.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAB41026.1	AB047099	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
BAB41024.1	AB047097	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
BAB41022.1	AB047095	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1	AB047093	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAA89008.1	AB027454	Petunia x hybrida anthocyanidin 3-O-glucosyltransferase. PGT8.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.
CAB56231.1	Y1S871	Dorotheanthus bellidiformis betanidin-5-O-glucosyltransferase.

AAB81683.1	AF000372	Vitis vinifera UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41019.1	AB047092	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41025.1	AB047098	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FlUFGT1.
BAB41023.1	AB047096	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT1.
BAB41021.1	AB047094	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
AAB81682.1	AF000371	Vitis vinifera UDP glucose:flavonoid 3-o-glucosyltransferase.
BAA19659.1	AB002818	Perilla frutescens flavonoid 3-O-glucosyltransferase. UDP glucose.
BAA90787.1	AB038248	Ipomoea batatas UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.
AAD04166.1	AF101972	Phaseolus lunatus catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
AAB86473.1	AF028237	Ipomoea purpurea UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
SEQ ID NO: 900		
AAA33975.1	M11395	Glycine max small heat shock protein.
CAA41547.1	X58711	Medicago sativa heat shock protein.
AAB03893.1	M11318	Glycine max 17.5 kd heat shock protein Gmhsp17.6L.
AAA33672.1	M33899	Pisum sativum 18.1 kDa heat shock protein (hsp18.1).
CAA25578.1	X01104	Glycine max heat shock protein 6871 (aa 1-153).
CAB55634.2	AJ237596	Helianthus annuus 17.9 kDa heat-shock protein. hsp17.9.
BAA33062.1	AB017273	Cuscuta japonica low-molecular-weight heat shock protein. CJHSP17.
AAA33974.1	M11317	Glycine max 17.6 kd heat shock protein Gmhsp17.6L.
AAD30454.1	AF123257	Lycopersicon esculentum 17.6 kD class I small heat shock protein. HSP17.6.
AAD30452.1	AF123255	Lycopersicon esculentum 17.7 kD class I small heat shock protein. HSP17.7.

CAA39603.1	X56138	<i>Lycopersicon esculentum</i> small heat shock protein (class I).
AAD30453.1	AF123256	<i>Lycopersicon esculentum</i> 17.8 kD class I small heat shock protein. HSP17.8.
CAA37847.1	X53851	<i>Daucus carota</i> heat shock protein.
AAA33671.1	M33900	<i>Pisum sativum</i> 17.9 kDa heat shock protein (hsp17.9).
AAF34133.1	AF161179	<i>Malus x domestica</i> low molecular weight heat shock protein. Hsp1.
CAA41546.1	X58710	<i>Medicago sativa</i> heat shock protein.
AAB63310.1	U46544	<i>Helianthus annuus</i> 18.6 kDa heat-shock protein. Class I low-molecular-weight heat-shock protein.
AAB63311.1	U46545	<i>Helianthus annuus</i> 17.7 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.
CAB08441.1	Z95153	<i>Helianthus annuus</i> 17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.
CAA42222.1	X59701	<i>Helianthus annuus</i> 17.6 kDa heat shock protein.
AAC39360.1	U63631	<i>Fragaria x ananassa</i> LMW heat shock protein.
AAA33910.1	M80939	<i>Oryza sativa</i> 16.9 kDa heat shock protein.
CAA37848.1	X53852	<i>Daucus carota</i> heat shock protein.
AAA33909.1	M80938	<i>Oryza sativa</i> 16.9 kDa heat shock protein.
CAA43210.1	X60820	<i>Oryza sativa</i> 16.9 KD low molecular weight heat shock protein.
CAA37864.1	X53870	<i>Chenopodium rubrum</i> heat-shock protein.
AAD49336.1	AF166277	<i>Nicotiana tabacum</i> low molecular weight heat-shock protein. LHS-1. TLHS-1.
AAA61632.1	U08601	<i>Papaver somniferum</i> low molecular weight heat-shock protein.
AAB72109.1	AF022217	<i>Brassica rapa</i> low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
CAA63902.1	X94192	<i>Pennisetum glaucum</i> heat shock protein 16.9. hsp16.9.
AAB39856.1	U81385	<i>Oryza sativa</i> heat shock protein. Oshsp16.9C. class I, low molecular mass.

CAA46641.1	X65725	Zea mays
heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.		
CAA08908.1	AJ009880	Castanea sativa
molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.		
CAB93512.1	AJ243565	Brassica oleracea
putative class I small heat shock protein. HSP17.7-a protein. hsp17.7-a.		
CAA63903.1	X94193	Pennisetum glaucum
heat shock protein 17.9. hsp17.9.		
CAB36910.1	AJ000691	Quercus suber
stress protein chaperone. heat shock protein 17.4. hsp17.		
CAA63901.1	X94191	Pennisetum glaucum
heat shock protein 17.0. hsp17.0.		
AAC78392.1	U83669	Oryza sativa
low molecular mass heat shock protein Oshsp17.3. OSHSP17.3. class I LMMHSP.		
BAA02160.1	D12635	Oryza sativa
'low molecular weight heat shock protein'.		
AAC78393.1	U83670	Oryza sativa
low molecular mass heat shock protein Oshsp18.0. OSHSP18.0. class I LMMHSP.		
CAA31785.1	X13431	Triticum aestivum
put. heat shock protein (AA 1 -151).		
CAA63570.1	X92983	Pseudotsuga menziesii
low molecular weight heat-shock protein.		
AAC78394.1	U83671	Oryza sativa
low molecular mass heat shock protein Oshsp17.7. OSHSP17.7. class I LMMHSP.		
CAA63571.1	X92984	Pseudotsuga menziesii
low molecular weight heat-shock protein.		
SEQ ID NO: 901		
AAG08959.1	AF122051	Solanum tuberosum
tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.		
AAG08960.1	AF122052	Solanum tuberosum
tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.		
AAG08961.1	AF122053	Solanum tuberosum
tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.		
AAF67053.1	AF190304	Adiantum raddianum
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.		
AAF67052.1	AF190303	Adiantum raddianum
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.		
AAF34434.1	AF172282	Oryza sativa
myb-like protein. DUPR11.29.		

AAF78888.1 AF189786 *Physcomitrella patens*  
putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.

AAF78887.1 AF189785 *Physcomitrella patens*  
putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.

AAF43043.1 AF236059 *Papaver rhoeas*  
putative Myb-related domain. pmr.

BAA94769.1 AP001859 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome 4, BAC clone F4D11; putative myb-protein.  
(AL022537).

AAF78890.1 AF189788 *Hordeum vulgare*  
putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.

AAF78889.1 AF189787 *Hordeum vulgare*  
putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.

BAA88169.1 AP000836 *Oryza sativa*  
Similar to putative transcription factor (AF062890).

BAA88205.1 AP000837 *Oryza sativa*  
Similar to putative transcription factor (AF062890).

CAA78388.1 Z13998 *Petunia x hybrida*  
DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb  
proto-oncoproteins.

AAF67051.1 AF190302 *Secale cereale*  
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.

AAF67050.1 AF190301 *Secale cereale*  
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.

AAG28525.1 AF198498 *Nicotiana tabacum*  
anther-specific myb-related protein 2. mybAS2. NtMYBAS2; contains tandem R2, R3 myb  
domains similar to c-myb family.

BAB12688.1 AP002746 *Oryza sativa*  
putative MYB family transcription factor. P0671B11.3. contains ESTs  
AU082307(E0784),C72014(E0784).

BAA99440.1 AP002743 *Oryza sativa*  
putative MYB family transcription factor. P0710E05.27. contains ESTs  
AU082307(E0784),C72014(E0784).

AAK19619.1 AF336286 *Gossypium hirsutum*  
GHMYB9. ghmyb9. similar to myb.

CAA64615.1 X95297 *Lycopersicon esculentum*  
transcription factor. THM1. myb-related.

BAA81730.1 AB029159 *Glycine max*  
GmMYB29A1.

CAA50224.1 X70879 *Hordeum vulgare*  
MybHv1. myb1.

CAA50222.1 X70877 *Hordeum vulgare*  
MybHv1. myb1.

CAB40189.1	AJ133638	Avena sativa transcriptional activator. myb protein. gamyb.
AAG28526.1	AF198499	Nicotiana tabacum anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
AAD31395.1	AF114162	Lolium temulentum gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.
BAA81732.1	AB029161	Glycine max GmMYB29A2.
BAA81731.1	AB029160	Glycine max GmMYB29A1.
CAA61021.1	X87690	Hordeum vulgare transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
AAG22863.1	AY008692	Hordeum vulgare transcription factor GAMyb. Gamyb.
BAA96421.1	AB044084	Triticum aestivum transcription activator for gibberellin response. GAMyb protein. Ta-GAMyb.
BAA81733.2	AB029162	Glycine max GmMYB29A2.
BAA81736.1	AB029165	Glycine max GmMYB29B2.
AAA33067.1	L04497	Gossypium hirsutum MYB A; putative.
BAB39972.1	AP003018	Oryza sativa putative transcription factor (myb). OSJNBA0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
CAA72218.1	Y11415	Oryza sativa myb.
CAA67000.1	X98355	Oryza sativa activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
BAB39987.1	AP003020	Oryza sativa putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
CAA78387.1	Z13997	Petunia x hybrida DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
CAA72217.1	Y11414	Oryza sativa myb.
BAA23341.1	D88621	Oryza sativa transfactor. OSMYB5. Osmyb5.

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BAA93038.1 AP001552 *Oryza sativa*

EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* putative transcription factor (AF062916).

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CAA64614.1 X95296 *Lycopersicon esculentum*  
transcription factor. THM27. myb-related.

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AAK19616.1 AF336283 *Gossypium hirsutum*

GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.

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CAA78386.1 Z13996 *Petunia x hybrida*

DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.

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CAA67575.1 X99134 *Lycopersicon esculentum*  
transcription factor. THM6. myb-related.

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BAA88222.1 AB028650 *Nicotiana tabacum*  
myb-related transcription factor LBM2. lbm2.

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SEQ ID NO: 902

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CAA57773.1 X82329 *Arachis hypogaea*  
chitinase (class II). chi2;1.

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AAD54935.1 AF141373 *Petroselinum crispum*  
random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-1. class II.

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AAD54936.1 AF141374 *Petroselinum crispum*  
random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-2. class II.

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AAF00131.1 AF147091 *Fragaria x ananassa*  
chitin degradation. class II chitinase. Chi2-1.

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AAC95376.1 AF105426 *Cynodon dactylon*  
chitinase. Cht2.

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BAA95846.1 AP002070 *Oryza sativa*  
Similar to *Oryza sativa* clone RGCH7 chitinase. (AF013581).

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AAA32986.1 M95835 *Brassica napus*  
endochitinase. Ch25.

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AAF69783.1 AF135143 *Arabis lemmonii*  
class I chitinase.

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AAF69775.1 AF135135 *Arabis drummondii*  
class I chitinase.

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AAF69792.1 AF135152 *Arabis parishii*  
class I chitinase.

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AAC95375.1 AF105425 *Cynodon dactylon*  
chitinase. Cht1.

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AAF69785.1 AF135145 *Arabis lignifera*  
class I chitinase.

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AAF69770.1 AF135130 *Arabis holboellii*

class I chitinase.

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AAF69781.1 AF135141 *Arabis gunnisoniana*

class I chitinase.

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AAF69777.1 AF135137 *Arabis fecunda*

class I chitinase.

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AAF69790.1 AF135150 *Arabis microphylla*

class I chitinase.

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AAF69787.1 AF135147 *Arabis lignifera*

class I chitinase.

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AAF69772.1 AF135132 *Arabis gunnisoniana*

class I chitinase.

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AAF69782.1 AF135142 *Halimolobos perplexa* var. *perplexa*

class I chitinase.

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AAF69784.1 AF135144 *Arabis lemmonii*

class I chitinase.

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AAF69788.1 AF135148 *Arabis lyallii*

class I chitinase.

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BAA03750.1 D16222 *Oryza sativa*

endochitinase. Cht-2.

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AAF69776.1 AF135136 *Arabis fecunda*

class I chitinase.

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CAA40107.1 X56787 *Oryza sativa*

chitinase.

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BAB13369.1 AB048531 *Psophocarpus tetragonolobus*

class I chitinase.

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AAF69778.1 AF135138 *Arabis glabra*

class I chitinase.

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AAF69786.1 AF135146 *Arabis lignifera*

class I chitinase.

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BAA82826.1 AB023464 *Arabis gemmifera*

basic endochitinase. ChiB.

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AAF69773.1 AF135133 *Arabis blepharophylla*

class I chitinase.

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AAF69791.1 AF135151 *Arabis microphylla*

class I chitinase.

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AAF69793.1 AF135153 *Arabis parishii*

class I chitinase.

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CAA39535.1 X56063 *Oryza sativa*

chitinase.

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BAA03749.1 D16221 *Oryza sativa*

endochitinase. Cht-1.

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AAF69789.1 AF135149 *Arabis microphylla*  
class I chitinase.

CAA71402.1 Y10373 *Medicago truncatula*  
chitinase.

AAC16010.1 AF061805 *Elaeagnus umbellata*  
acidic chitinase.

CAA53626.1 X76041 *Triticum aestivum*  
endochitinase. CHI.

BAA33971.1 AB008892 *Nicotiana tabacum*  
chitinase 134. Chn134.

CAA47921.1 X67693 *Solanum tuberosum*  
chitinase. SK2. endochitinase.

AAF69780.1 AF135140 *Arabis glabra*  
class I chitinase.

BAB18519.1 AB051578 *Secale cereale*  
seed chitinase-a. rsca.

AAA51377.1 L37289 *Oryza sativa*  
chitinolytic activity, antifungal activity. chitinase.

AAB41324.1 U83591 *Medicago sativa*  
class I chitinase.

CAC17793.1 AJ301671 *Nicotiana sylvestris*  
hydrolysis of chitin. endochitinase. chnb. class I chitinase.

AAB41325.1 U83592 *Medicago sativa*  
class I chitinase.

AAB23263.1 S43926 *Phaseolus vulgaris*  
chitinase. CH5B. This sequence comes from Fig. 1.

AAA33756.1 M13968 *Phaseolus vulgaris*  
chitinase (EC 3.2.1.14).

CAA35945.1 X51599 *Nicotiana tabacum*  
chitinase. CHN50.

AAA34070.1 M15173 *Nicotiana tabacum*  
endochitinase precursor (EC 3.2.1.14).

CAA45822.1 X64519 *Nicotiana tabacum*  
chitinase B class I. CHN200.

SEQ ID NO: 903

BAA78764.1 AB023482 *Oryza sativa*  
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar  
to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAF43496.1 AF131222 *Lophopyrum elongatum*  
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and  
ABA treatment.

AAK11674.1 AF339747 *Lophopyrum elongatum*  
protein kinase. ESI47.

AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
BAA94509.1	AB041503	Populus nigra protein kinase 1. PnPK1.
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA94510.1	AB041504	Populus nigra protein kinase 2. PnPK2.
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB03429.1	AP002817	Oryza sativa EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
CAB51834.1	00069	Oryza sativa I1332.5. contains eukaryotic protein kinase domain PF.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
AAG03090.1	AC073405	Oryza sativa Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAB19337.1	AP003044	Oryza sativa putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
BAA90808.1	AP001168	Oryza sativa Similar to putative receptor-like protein kinase (AL035679).
AAG59657.1	AC084319	Oryza sativa putative protein kinase. OSJNBa0004B24.20.
AAB47424.1	U59317	Lycopersicon pimpinellifolium serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.

AAC48932.1 U13923 *Lycopersicon pimpinellifolium*  
Fen. putative serine/threonine protein kinase; similar to product encoded by *Lycopersicon pimpinellifolium* Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.

AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*  
Fen kinase.

BAA92221.1 AP001278 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).

BAA87852.1 AP000816 *Oryza sativa*  
Similar to putative Ser/Thr protein kinase. (AC004218).

AAB61708.1 U93048 *Daucus carota*  
somatic embryogenesis receptor-like kinase. SERK.

AAK11566.1 AF318490 *Lycopersicon hirsutum*  
Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.

AAK11568.1 AF318492 *Lycopersicon hirsutum*  
Pto-like protein kinase B. LhirPtoB.

AAD21872.1 AF078082 *Phaseolus vulgaris*  
receptor-like protein kinase homolog RK20-1.

AAF66615.1 AF142596 *Nicotiana tabacum*  
LRR receptor-like protein kinase.

AAC23542.1 U20948 *Ipomoea trifida*  
receptor protein kinase. IRK1.

AAF91337.1 AF249318 *Glycine max*  
Ptl1 kinase-like protein. Ptl1b. protein kinase.

AAC27894.1 AF023164 *Zea mays*  
leucine-rich repeat transmembrane protein kinase 1. ltk1.

AAF76314.1 AF220603 *Lycopersicon esculentum*  
Fen kinase. Lescfen.

AAB47422.1 U59318 *Lycopersicon esculentum*  
serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.

AAF76313.1 AF220603 *Lycopersicon esculentum*  
Pto kinase. LescPth5.

AAB47421.1 U59316 *Lycopersicon esculentum*  
serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

AAF91336.1 AF249317 *Glycine max*  
Ptl1 kinase-like protein. Ptl1a. protein kinase.

AAK11567.1 AF318491 *Lycopersicon hirsutum*  
Pto-like protein kinase F. LhirPtoF.

AAC61805.1 U28007 *Lycopersicon esculentum*  
serine/threonine protein kinase. Pto kinase interactor 1. Pt1. Pt1 kinase.

AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.
AAF76306.1	AF220602	Lycopersicon pimpinellifolium Pto kinase.
AAB47423.1	U59315	Lycopersicon pimpinellifolium serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
BAB21241.1	AP002953	Oryza sativa Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
AAC48914.1	U02271	Lycopersicon pimpinellifolium protein kinase.
SEQ ID NO: 904		
AAF65545.1	AF233894	Perilla citriodora limonene synthase.
AAG31437.1	AF241792	Perilla frutescens limonene synthase.
AAK06663.1	AF317695	Perilla frutescens var. frutescens limonene synthase.
AAG31435.1	AF241790	Perilla citriodora limonene synthase.
BAA21629.1	AB005744	Perilla frutescens catalyzing the cyclization of geranyl pyrophosphate to 1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ Acc#D49368.
AAG31438.1	AF241793	Perilla frutescens limonene synthase.
BAA08367.1	D49368	Perilla frutescens limonene cyclase.
AAC37366.1	L13459	Mentha spicata 4S-limonene synthase.
AAD50304.1	AF175323	Mentha longifolia limonene synthase. monoterpene synthase.
AAG01140.1	AF282875	Schizonepeta tenuifolia (+)-4R-limonene synthase.
AAF21053.1	AF212433	Capsicum annuum UV-induced sesquiterpene cyclase. SC2.

BAA82141.1 AB023816 Solanum tuberosum  
vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.

AAF74977.1 AF270425 Gossypium hirsutum  
(E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene synthase. cdn2. sesquiterpene cyclase.

BAA82092.1 AB022598 Solanum tuberosum  
vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.

BAA82109.1 AB022720 Solanum tuberosum  
vetispiradiene synthase. PVS3. potato sesquiterpene cyclase; PVS3.

AAG09949.1 AF171216 Lycopersicon esculentum  
vetispiradiene synthase. LEVS2. sesquiterpene cyclase.

BAA82108.1 AB022719 Solanum tuberosum  
vetispiradiene synthase. PVS2. potato sesquiterpene cyclase; PVS2.

AAC12784.1 U88318 Gossypium hirsutum  
(E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.

AAK15641.1 AF326117 Capsicum annuum  
sesquiterpene cyclase. PSC2.

AAC61260.1 AF061285 Capsicum annuum  
sesquiterpene cyclase. UV induced.

AAG24640.2 AF304444 Artemisia annua  
sesquiterpene cyclase.

CAC12731.1 AJ271792 Artemisia annua  
putative sesquiterpene cyclase. cASC125.

SEQ ID NO: 905

AAF64450.1 AF239928 Euphorbia esula  
glutathione S-transferase. similar to auxin-inducible GST.

AAG34803.1 AF243368 Glycine max  
glutathione S-transferase GST 13.

AAG16759.1 AY007561 Lycopersicon esculentum  
putative glutathione S-transferase T4.

AAG34798.1 AF243363 Glycine max  
glutathione S-transferase GST 8.

AAG34797.1 AF243362 Glycine max  
glutathione S-transferase GST 7.

AAG16758.1 AY007560 Lycopersicon esculentum  
putative glutathione S-transferase T3.

AAG34809.1 AF243374 Glycine max  
glutathione S-transferase GST 19.

AAG34801.1 AF243366 Glycine max  
glutathione S-transferase GST 11.

AAG34796.1 AF243361 Glycine max  
glutathione S-transferase GST 6.

AAG34807.1 AF243372 Glycine max  
glutathione S-transferase GST 17.

AAG16757.1 AY007559 Lycopersicon esculentum  
putative glutathione S-transferase T2.

AAG16756.1 AY007558 Lycopersicon esculentum  
putative glutathione S-transferase T1.

AAG34804.1 AF243369 Glycine max  
glutathione S-transferase GST 14.

AAG34810.1 AF243375 Glycine max  
glutathione S-transferase GST 20.

AAG34808.1 AF243373 Glycine max  
glutathione S-transferase GST 18.

AAG34805.1 AF243370 Glycine max  
glutathione S-transferase GST 15.

AAG34844.1 AF244701 Zea mays  
glutathione S-transferase GST 36.

AAG34829.1 AF244686 Zea mays  
glutathione S-transferase GST 21.

AAG34831.1 AF244688 Zea mays  
glutathione S-transferase GST 23.

AAA68430.1 J03679 Solanum tuberosum  
glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.

AAC18566.1 AF048978 Glycine max  
2,4-D inducible glutathione S-transferase. GSTa.

AAG34832.1 AF244689 Zea mays  
glutathione S-transferase GST 24.

AAG34800.1 AF243365 Glycine max  
glutathione S-transferase GST 10.

AAG34849.1 AF244706 Zea mays  
glutathione S-transferase GST 41.

AAG34837.1 AF244694 Zea mays  
glutathione S-transferase GST 29.

AAC32118.1 AF051214 Picea mariana  
probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.

AAG41204.1 AF321437 Suaeda maritima  
glutathione transferase.

AAG34802.1 AF243367 Glycine max  
glutathione S-transferase GST 12.

AAF29773.1 AF159229 Gossypium hirsutum  
glutathione S-transferase. GST.

AAG32472.1 AF309379 Oryza sativa subsp. japonica  
putative glutathione S-transferase OsGSTU3.

AAG34836.1 AF244693 Zea mays  
 glutathione S-transferase GST 28.  
 CAA04391.1 AJ000923 Carica papaya  
 glutathione transferase. PGST1.  
 CAA71784.1 Y10820 Glycine max  
 glutathione transferase.  
 CAA09187.1 AJ010448 Alopecurus myosuroides  
 glutathione transferase. GST1a.  
 AAG34795.1 AF243360 Glycine max  
 glutathione S-transferase GST 5.  
 CAA09188.1 AJ010449 Alopecurus myosuroides  
 glutathione transferase. GST1b.  
 AAG34806.1 AF243371 Glycine max  
 glutathione S-transferase GST 16.  
 CAC24549.1 AJ296343 Cichorium intybus x Cichorium endivia  
 glutathione S-transferase. chi-GST1. auxin-induced GST.  
 AAC28101.1 AF079511 Mesembryanthemum crystallinum  
 glutathione S-transferase.

SEQ ID NO: 907

AAA33280.1 L20475 Datura stramonium  
 29kDa protein; high homology to aa sequence of tropinone reductases.  
 AAA33281.1 L20473 Datura stramonium  
 catalyses a stereospecific reduction of tropinone to tropine. tropinone reductase-I.  
 CAC34420.1 AJ307584 Solanum tuberosum  
 tropine forming tropinone reductase. tropinone reductase I. TRI.  
 BAA85844.1 AB026544 Hyoscyamus niger  
 tropinone reductase-I. tr1.  
 BAA13547.1 D88156 Hyoscyamus niger  
 tropinone reductase-I.  
 AAA33282.1 L20474 Datura stramonium  
 catalyses a stereospecific reduction of tropinone to pseudotropine. tropinone reductase-II.  
 AAB09776.1 L20485 Hyoscyamus niger  
 tropinone reductase-II.  
 BAA85845.1 AB026545 Hyoscyamus niger  
 tropinone reductase-II. tr2.  
 CAB52307.1 AJ245634 Solanum tuberosum  
 pseudotropine forming tropinone reductase. tropinone reductase II. TRII.  
 CAC19810.1 AJ292343 Solanum tuberosum  
 pseudotropine forming tropinone reductase. tropinone reductase II. trII.  
 CAA45866.1 X64566 Cuphea lanceolata  
 beta-ketoacyl-ACP reductase. Clkr27. 3-oxoacyl-[acyl-carrier protein] reductase.

CAA45793.1 X64463 Brassica napus  
3-oxoacyl-[acyl-carrier protein] reductase.

AAB82767.1 U89509 Zea mays  
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAB82766.1 U89510 Hordeum vulgare  
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

CAA74176.1 Y13861 Nicotiana tabacum  
enoyl-ACP reductase. enr-T2.

AAB20114.2 S60064 Brassica napus  
enoyl-acyl carrier protein reductase. This sequence comes from fig3; conceptual translation  
differs from published sequence.

CAA74177.1 Y13862 Nicotiana tabacum  
enoyl-ACP reductase. enr-T1.

AAC78100.1 AF093628 Oryza sativa  
protochlorophyllide reductase homolog.

CAA05879.1 AJ003124 Petunia x hybrida  
enoyl-ACP reductase. pte.

CAA64729.1 X95462 Brassica napus  
enoyl reductase.

CAA05816.1 AJ003025 Oryza sativa  
enoyl-ACP reductase.

BAA99570.1 AB036823 Chlorella vulgaris  
oxidoreductase. oxi.

SEQ ID NO: 909

BAA82107.1 AB022693 Nicotiana tabacum  
transcription factor. NtWRKY1.

AAC31956.1 AF080595 Pimpinella brachycarpa  
zinc finger protein. ZFP1. WRKY1.

AAD55974.1 AF121353 Petroselinum crispum  
zinc-finger type transcription factor WRKY1. WRKY1.

BAA77383.1 AB020590 Nicotiana tabacum  
transcription factor NtWRKY2.

AAC49527.1 U48831 Petroselinum crispum  
WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

AAD32677.1 AF140554 Avena sativa  
DNA-binding protein WRKY1. wrky1. putative transcription factor.

CAA88326.1 Z48429 Avena fatua  
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

AAD16139.1 AF096299 Nicotiana tabacum  
DNA-binding protein 2. WRKY2. transcription factor.

BAA86031.1 AB026890 Nicotiana tabacum  
transcription factor NtWRKY4.

AAC37515.1 L44134 *Cucumis sativus*  
SPF1-like DNA-binding protein.

AAK16171.1 AC079887 *Oryza sativa*  
putative DNA-binding protein. OSJNBa0040E01.10.

AAF23898.1 AF193802 *Oryza sativa*  
zinc finger transcription factor WRKY1.

AAD16138.1 AF096298 *Nicotiana tabacum*  
DNA-binding protein 1. WRKY1. transcription factor.

AAC49529.1 U58540 *Petroselinum crispum*  
WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.

CAB97004.1 AJ278507 *Solanum tuberosum*  
putative transcription factor. WRKY DNA binding protein. WRKY1.

BAB19075.1 AP002744 *Oryza sativa*  
putative DNA-binding protein homolog. P0006C01.17.

BAB19096.1 AP002839 *Oryza sativa*  
putative DNA-binding protein homolog. P0688A04.2.

AAK16170.1 AC079887 *Oryza sativa*  
putative DNA binding protein. OSJNBa0040E01.4.

BAB40073.1 AP003074 *Oryza sativa*  
putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).

AAD38283.1 AC007789 *Oryza sativa*  
putative WRKY DNA binding protein. OSJNBa0049B20.9.

BAB18313.1 AP002865 *Oryza sativa*  
putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).

CAA88331.1 Z48431 *Avena fatua*  
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

AAC49528.1 U56834 *Petroselinum crispum*  
DNA-binding. WRKY3. WRKY-type DNA-binding protein.

AAG35658.1 AF204925 *Petroselinum crispum*  
transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.

BAB16432.1 AB041520 *Nicotiana tabacum*  
WRKY transcription factor Nt-SubD48. Nt-SubD48.

AAD32676.1 AF140553 *Avena sativa*  
DNA-binding protein WRKY3. wrky3. putative transcription factor.

AAG46150.1 AC018727 *Oryza sativa*  
putative DNA-binding protein. OSJNBa0056G17.18.

BAA77358.1 AB020023 *Nicotiana tabacum*  
WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.

AAG35659.1 AF204926 *Petroselinum crispum*  
transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.

AAD27591.1 AF121354 *Petroselinum crispum*  
binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.

CAB66338.1 AJ279697 *Betula pendula*  
wrky-type DNA binding protein. wrky.

AAF61864.1 AF193771 *Nicotiana tabacum*  
DNA-binding protein 4. WRKY4. transcription factor.

BAA87069.1 AB035271 *Matricaria chamomilla*  
elicitor-induced DNA-binding protein homolog. McWRKY1.

AAF61863.1 AF193770 *Nicotiana tabacum*  
DNA-binding protein 3. WRKY3. transcription factor.

SEQ ID NO: 910

AAC09420.1 M68929 Mitochondrion *Marchantia polymorpha*  
rps14.

CAA33994.1 X15901 Plastid *Oryza sativa*  
ribosomal protein S14. rps14.

SEQ ID NO: 911

CAA55128.1 X78325 *Nicotiana tabacum*  
chitinase/lysozyme. Pz.

CAA54373.1 X77110 *Nicotiana tabacum*  
chitinase, class V. chi-V.

CAA54374.1 X77111 *Nicotiana tabacum*  
chitinase, class V. chi-V.

SEQ ID NO: 912

CAB55394.1 AL117264 *Oryza sativa*  
zwh0010.1. similar to *Arabidopsis* germin-like protein 6 (AF032976); Method: conceptual translation with partial peptide sequencing.

BAA78563.1 AB024338 *Atriplex lentiformis*  
germin-like protein.

AAB97470.1 AF042489 *Oryza sativa*  
germin-like protein 16. glp16.

AAA33030.1 M93041 *Mesembryanthemum crystallinum*  
germin-like protein. germin-like protein.

CAB65371.1 AJ250834 *Pisum sativum*  
germin-like protein. ger2b. 2nd variant of the clone PsGER2.

CAB55559.1 AJ237943 *Triticum aestivum*  
germin-like protein. glp2b.

CAB65370.1 AJ250833 *Pisum sativum*  
germin-like protein. ger2a. 1st variant of this clone.

CAB55558.1 AJ237942 *Triticum aestivum*  
germin-like protein. glp2a.

AAD43971.1 AF141878 *Oryza sativa*  
germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

AAD43973.1 AF141880 *Oryza sativa*  
germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

AAC04837.1 AF032976 *Oryza sativa*  
germin-like protein 6. GER6. similar to wheat and barley oxalate oxidase.

AAG00425.1 AF250933 *Hordeum vulgare*  
germin A. GerA. apoplastic protein; contains prepeptide for targeting into the cell wall.

AAD43972.1 AF141879 *Oryza sativa*  
germin-like protein 2 precursor. RGLP2. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

CAA63659.1 X93171 *Hordeum vulgare*  
oxalate oxidase-like protein or germin-like protein.

AAC04833.1 AF032972 *Oryza sativa*  
germin-like protein 2. GER2. similar to wheat and barley oxalate oxidase.

AAC04834.1 AF032973 *Oryza sativa*  
germin-like protein 3. GER3. similar to wheat and barley oxalate oxidase.

AAC04832.1 AF032971 *Oryza sativa*  
germin-like protein 1. GER1. similar to wheat and barley oxalate oxidase.

AAG00426.1 AF250934 *Hordeum vulgare*  
germin B. GerB. apoplastic protein; contains prepeptide for targeting into the cell wall.

AAG00427.1 AF250935 *Hordeum vulgare*  
germin F. GerF. apoplastic protein; contains prepeptide for targeting into the cell wall.

AAF34811.1 AF005084 *Triticum aestivum*  
oxalate oxidase. up-regulated by aluminum.

AAC04835.1 AF032974 *Oryza sativa*  
germin-like protein 4. GER4. similar to wheat and barley oxalate oxidase.

BAB39965.1 AP003018 *Oryza sativa*  
probable germin protein 4. OSJNBa0004B13.19. contains ESTs  
AU101991(S4037),AU070167(R0031).

BAB39980.1 AP003020 *Oryza sativa*  
probable germin protein 4. P0498A12.8. contains ESTs  
AU101991(S4037),AU070167(R0031).

AAG00428.1 AF250936 *Hordeum vulgare*  
germin D. GerD. apoplastic protein; contains prepeptide for targeting into the cell wall.

AAA20245.1 U01963 *Hordeum vulgare*  
germin subunit.

CAC19429.1 AJ291825 *Lolium perenne*  
oxalate oxidase. oxO1.

AAA34270.1 M63223 *Triticum aestivum*  
germin. germin 9f-2.8.

AAA34268.1 M21962 *Triticum aestivum*  
germin protein precursor.

CAA74595.1	Y14203	Hordeum vulgare oxalate oxidase.
AAG00429.1	AF250937	Hordeum vulgare germin E. GerE. apoplastic protein.
CAB65369.1	AJ250832	Pisum sativum germin-like protein. ger1.
AAA32959.1	L15737	Hordeum vulgare oxalate oxidase. This is the sequence of the complete mature peptide.
CAA71052.1	Y09917	Triticum aestivum germin homolog. pSBGer3.
AAA34271.1	M63224	Triticum aestivum germin. germin 9f-3.8.
CAA71050.1	Y09915	Triticum aestivum germin homolog. pSBGer1.
BAB18339.1	AP002865	Oryza sativa putative germin protein. P0034C11.30. contains EST C97263(C53484).
AAD38298.1	AC007789	Oryza sativa putative oxalate oxidase (germin protein). OSJNBa0049B20.25.
BAA86880.1	AB028454	Barbula unguiculata germin-like protein.
AAF03355.1	AF132671	Nicotiana plumbaginifolia nectarin I precursor. NEC1. germin-like protein.
BAA25197.1	AB012138	Lycopersicon esculentum adaptation to Mn-deficiency. germin-like protein. Mdip1.
AAC78470.1	AF067731	Solanum tuberosum germin-like protein. OXAOXA. similar to oxalate oxidase.
AAC25777.1	AF072694	Oryza sativa germin-like protein 7. GER7. similar to wheat and barley oxalate oxidase.
AAC99473.1	AF039201	Pinus caribaea germin-like protein. PcGER1.
CAA71051.1	Y09916	Triticum aestivum germin homolog. pSBGer2.
AAC05146.1	AF049065	Pinus radiata germin-like protein. PRGer1.
CAC34417.1	AJ311624	Pisum sativum Germin-like protein. glp3.
SEQ ID NO: 915		
BAB19363.1	AP002542	Oryza sativa putative beta-1,3-glucanase. P0679C08.2.
AAD10386.1	U72255	Oryza sativa beta-1,3-glucanase precursor. Gns9.

CAB85903.1	AJ251646	<i>Pisum sativum</i> hydrolysis of beta-1,3 conjugated glucans. beta-1,3 glucanase. gns2.
AAA90953.1	U30323	<i>Triticum aestivum</i> beta 1,3-glucanase. Glc1.
BAA89481.1	AB029462	<i>Salix gilgiana</i> beta-1,3-glucanase. SgGN1.
BAB40807.1	AB052291	<i>Pyrus pyrifolia</i> catalyzing the hydrolysis of 1,3-beta-glucosyl linkages. endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the protein(BGN-1) encoded by pear pollen bgn-1 with barley endo-1,3-beta-glucanase(GII. accession number: pdb/1GHS-B/2.3/2/306/N/)(40% identity) and their hydrophobic cluster analysis(HCA)(a overall HCA homology score of 87.1%) showed that it was most likely that the bgn-1 encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession number: dad/AJ251646-1).
AAB82772.2	AF001523	<i>Musa acuminata</i> beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
CAA49513.1	X69887	<i>Brassica napus</i> beta-1,3-glucanase homologue.
AAF08679.1	AF004838	<i>Musa acuminata</i> beta-1,3-glucanase.
CAA82271.1	Z28697	<i>Nicotiana tabacum</i> beta-1,3-glucanase.
AAD10384.1	U72253	<i>Oryza sativa</i> beta-1,3-glucanase precursor. Gns7.
CAB71021.1	AJ271598	<i>Hieracium piloselloides</i> putative role in callose degradation. putative beta-1,3-glucanase. gluc.
CAA30261.1	X07280	<i>Nicotiana plumbaginifolia</i> beta-glucanase.
AAA51643.1	M23120	<i>Nicotiana plumbaginifolia</i> beta-glucanase precursor.
AAA87456.1	U22147	<i>Hevea brasiliensis</i> beta-1,3-glucanase. HGN1. hydrolytic enzyme.
AAA34078.1	M63634	<i>Nicotiana plumbaginifolia</i> regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
AAD10385.1	U72254	<i>Oryza sativa</i> beta-1,3-glucanase precursor. Gns8.
CAB38443.1	AJ133470	<i>Hevea brasiliensis</i> beta-1,3-glucanase. hgn1.
AAB03501.1	U41323	<i>Glycine max</i> beta-1,3-glucanase. SGN1.
AAA32939.1	M62907	<i>Hordeum vulgare</i> hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase. cBGL32.

AAD33881.1	AF141654	Nicotiana tabacum beta-1,3-glucanase. GGL4.
AAA03617.1	M80604	Lycopersicon esculentum beta-1,3-glucanase.
BAA77786.1	AB027431	Oryza sativa beta-1,3-glucanase.
BAA77787.1	AB027432	Oryza sativa beta-1,3-glucanase.
CAB91554.1	AJ277900	Vitis vinifera beta 1-3 glucanase. gl1.
AAC14399.1	AF030771	Hordeum vulgare beta-1,3-glucanase 2. BGL32.
CAA03908.1	AJ000081	Citrus sinensis glucan hydrolase. beta-1,3-glucanase. gns1.
AAG24921.1	AF311749	Hevea brasiliensis beta-1,3-glucanase.
AAA33946.1	M37753	Glycine max beta-1,3-endoglucanase (EC 3.2.1.39).
AAA63542.1	M59443	Nicotiana tabacum acidic beta-1,3-glucanase. glucanase.
AAD28732.1	AF112965	Triticum aestivum beta-1,3-glucanase precursor. Glb3.
AAD10381.1	U72250	Oryza sativa beta-1,3-glucanase precursor. Gns4.
CAA57255.1	X81560	Nicotiana tabacum (1-)beta-glucanase. Sp41a.
AAD33880.1	AF141653	Nicotiana tabacum beta-1,3-glucanase. GGL1.
AAB86541.1	AF030166	Oryza sativa glucanase. glu1.
AAA63539.1	M60402	Nicotiana tabacum glucan beta-1,3-glucanase. glucanase GLA.
AAA34053.1	M60464	Nicotiana tabacum beta-1,3-glucanase.
AAD10380.1	U72249	Oryza sativa beta-1,3-glucanase precursor. Gns3.
AAA63540.1	M60403	Nicotiana tabacum glucan-1,3-beta-glucosidase. glucanase GLB.
SEQ ID NO: 916		
AAA85440.1	U32624	Sorghum bicolor cytochrome P-450. CYP79. P450TYR; N-hydroxylase.

AAF27289.1 AF140613 *Manihot esculenta*  
N-hydroxylating cytochrome P450. CYP79D1.

AAF27290.1 AF140614 *Manihot esculenta*  
N-hydroxylating cytochrome P450. CYP79D2.

AAD03415.1 AF069494 *Sinapis alba*  
converts tyrosine to para-hydrophenylacetaldoxime in para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.

AAG59648.1 AC084319 *Oryza sativa*  
putative cytochrome p450tyr. OSJNBa0004B24.15.

AAF66543.1 AF140609 *Triglochin maritimum*  
cytochrome P450 CYP79E1. CYP79E1.

AAF66544.1 AF140610 *Triglochin maritimum*  
cytochrome P450 CYP79E2. CYP79E2.

BAA92894.1 AB006790 *Petunia x hybrida*  
cytochrome P450. IMT-2.

AAB94587.1 AF022458 *Glycine max*  
CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

AAC32274.1 AF081575 *Petunia x hybrida*  
flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.

AAD56282.1 AF155332 *Petunia x hybrida*  
flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

CAA64635.1 X95342 *Nicotiana tabacum*  
cytochrome P450. hsr515. hypersensitivity-related gene.

CAA50155.1 X70824 *Solanum melongena*  
flavonoid hydroxylase (P450). CYP75.

AAG44132.1 AF218296 *Pisum sativum*  
cytochrome P450. P450 isolog.

AAA32913.1 M32885 *Persea americana*  
cytochrome P-450LXXIA1 (cyp71A1).

BAA84071.1 AB028151 *Antirrhinum majus*  
flavone synthase II. cytochrome P450. AFNS2.

AAD38930.1 AF135485 *Glycine max*  
cytochrome P450 monooxygenaseCYP93D1. CYP93E1.

AAB17562.1 U72654 *Eustoma grandiflorum*  
flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

AAG34695.1 AF313492 *Matthiola incana*  
putative cytochrome P450.

CAA65580.1 X96784 *Nicotiana tabacum*  
cytochrome P450. hsr515.

BAA93634.1 AB025016 *Lotus japonicus*  
cytochrome P450.

CAA71513.1 Y10489 *Glycine max*  
putative cytochrome P450.

AAB94590.1	AF022461	Glycine max
		CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71876.1	Y10982	Glycine max
		putative cytochrome P450.
BAA12159.1	D83968	Glycine max
		Cytochrome P-450 (CYP93A1).
AAG14962.1	AF214008	Brassica napus
		cytochrome p450-dependent monooxygenase. BNF5H2.
BAA74465.1	AB022732	Glycyrrhiza echinata
		cytochrome P450. CYP Ge-31.
BAA22422.1	AB001379	Glycyrrhiza echinata
		cytochrome P450. CYP81E1.
AAG14961.1	AF214007	Brassica napus
		cytochrome p450-dependent monooxygenase. BNF5H1.
CAA04117.1	AJ000478	Helianthus tuberosus
		fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-race).
CAA04116.1	AJ000477	Helianthus tuberosus
		fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
AAB94593.1	AF022464	Glycine max
		CYP77A3p. CYP77A3. cytochrome P450 monooxygenase.
BAA13076.1	D86351	Glycine max
		cytochrome P-450 (CYP93A2).
CAA50647.1	X71656	Solanum melongena
		P450 hydroxylase.
SEQ ID NO: 918		
CAA06223.1	AJ004923	Lycopersicon esculentum
		Squalene epoxidase. ERG.
SEQ ID NO: 919		
AAF71823.1	AF153276	Populus tremula x Populus tremuloides
		pumilio domain-containing protein PPDI. PPD1. similar to Drosophila pumilio protein RNA-binding domain.
SEQ ID NO: 920		
BAA82393.1	AP000367	Oryza sativa
		EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).
CAC20842.1	AJ250467	Pinus sylvestris
		receptor protein kinase. upk.
AAB36558.1	U77888	Ipomoea nil
		receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
AAF91324.1	AF244890	Glycine max
		receptor-like protein kinase 3. RLK3. GmRLK3.

BAB40094.1 AP003210 *Oryza sativa*  
putative receptor protein kinase. OSJNBa0010K01.7.

AAF91322.1 AF244888 *Glycine max*  
receptor-like protein kinase 1. RLK1. GmRLK1.

AAC36318.1 AF053127 *Malus x domestica*  
leucine-rich receptor-like protein kinase. LRPKm1.

BAA84787.1 AP000559 *Oryza sativa*  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

BAA83373.1 AP000391 *Oryza sativa*  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

AAF59905.1 AF197946 *Glycine max*  
receptor protein kinase-like protein. CLV1A.

AAK27806.1 AC022457 *Oryza sativa*  
putative protein kinase. OSJNBa0006L06.21.

AAF91323.1 AF244889 *Glycine max*  
receptor-like protein kinase 2. RLK2. GmRLK2.

AAF34426.1 AF172282 *Oryza sativa*  
leucine rich repeat containing protein kinase. DUPR11.16.

AAK27817.1 AC022457 *Oryza sativa*  
putative protein kinase. OSJNBa0006L06.16.

CAA61510.1 X89226 *Oryza sativa*  
leucine-rich repeat/receptor protein kinase. l rk2.

BAB03621.1 AP002522 *Oryza sativa*  
putative protein kinase Xa21. P0009G03.21.

AAB82755.1 U72725 *Oryza longistaminata*  
receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.

BAB03629.1 AP002522 *Oryza sativa*  
putative protein kinase Xa21. P0009G03.30.

AAB61708.1 U93048 *Daucus carota*  
somatic embryogenesis receptor-like kinase. SERK.

AAF66615.1 AF142596 *Nicotiana tabacum*  
LRR receptor-like protein kinase.

AAB82756.1 U72724 *Oryza sativa*  
receptor kinase-like protein. Xa21 gene family member E.

CAB51480.1 Y14600 *Sorghum bicolor*  
putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

BAB39873.1 AP002882 *Oryza sativa*  
putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

BAB18321.1	AP002865	Oryza sativa putative receptor protein kinase. P0034C11.11.
BAB40081.1	AP003074	Oryza sativa putative receptor protein kinase. OSJNBa0004G10.30.
AAD38286.1	AC007789	Oryza sativa putative protein kinase. OSJNBa0049B20.13.
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAC27894.1	AF023164	Zea mays leucine-rich repeat transmembrane protein kinase 1. Itk1.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
AAG59657.1	AC084319	Oryza sativa putative protein kinase. OSJNBa0004B24.20.
BAA94519.1	AP001800	Oryza sativa ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4, BAC F9D16; putative receptor kinase (AL035394).
BAB07903.1	AP002835	Oryza sativa putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).
SEQ ID NO: 921		
BAA96250.1	AB027617	Pyrus pyrifolia UDP-glucose pyrophosphorylase.
BAA25917.1	AB013353	Pyrus pyrifolia UDP-glucose pyrophosphorylase.
CAA62689.1	X91347	Hordeum vulgare UDP-glucose pyrophosphorylase.
AAF62555.1	AF249880	Oryza sativa subsp. indica UDP-glucose pyrophosphorylase. UDPGase.
SEQ ID NO: 922		
AAD03415.1	AF069494	Sinapis alba converts tyrosine to para-hydrophenylacetaldoxime in para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.

AAA85440.1	U32624	Sorghum bicolor cytochrome P-450. CYP79. P450TYR; N-hydroxylase.
AAF27289.1	AF140613	Manihot esculenta N-hydroxylating cytochrome P450. CYP79D1.
AAF27290.1	AF140614	Manihot esculenta N-hydroxylating cytochrome P450. CYP79D2.
AAG59648.1	AC084319	Oryza sativa putative cytochrome p450tyr. OSJNBa0004B24.15.
AAF66543.1	AF140609	Triglochin maritimum cytochrome P450 CYP79E1. CYP79E1.
AAF66544.1	AF140610	Triglochin maritimum cytochrome P450 CYP79E2. CYP79E2.
BAA92894.1	AB006790	Petunia x hybrida cytochrome P450. IMT-2.
AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
CAA50155.1	X70824	Solanum melongena flavonoid hydroxylase (P450). CYP75.
AAC32274.1	AF081575	Petunia x hybrida flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.
AAG34695.1	AF313492	Matthiola incana putative cytochrome P450.
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.
AAB94587.1	AF022458	Glycine max CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAB17562.1	U72654	Eustoma grandiflorum flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
AAG09208.1	AF175278	Pisum sativum wound-inducible P450 hydroxylase. CYP82A1.
AAD37433.1	AF150881	Lycopersicon esculentum x Lycopersicon peruvianum catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.
CAA04117.1	AJ000478	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-race).
CAA04116.1	AJ000477	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

CAB43505.1	AJ239051	Cicer arietinum cytochrome P450. cyp81E2.
AAC49188.2	U29333	Pisum sativum cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAG14963.1	AF214009	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H3.
AAD38930.1	AF135485	Glycine max cytochrome P450 monooxygenaseCYP93D1. CYP93E1.
AAG14962.1	AF214008	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H2.
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAG14961.1	AF214007	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H1.
AAB94590.1	AF022461	Glycine max CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
BAA84071.1	AB028151	Antirrhinum majus flavone synthase II. cytochrome P450. AFNS2.
CAA50442.1	X71130	Petunia x hybrida P450 hydroxylase. PET 1.
SEQ ID NO: 924		
BAB20581.1	AB042268	Zea mays response regulator 6. ZmRR6.
AAK14395.1	AF339732	Dianthus caryophyllus response regulator protein. RR.
BAB20580.1	AB042267	Zea mays response regulator 5. ZmRR5.
BAB20579.1	AB042261	Zea mays response regulator 4. ZmRR4.
BAA85113.1	AB031012	Zea mays response regulator 2. ZmRR2. cytokinin-inducible.
BAA82873.1	AB024291	Zea mays response regulator. ZmRR2.
BAA75253.1	AB004882	Zea mays response regulator. ZmCip1, cytokinin-inducible protein.
BAA85112.1	AB031011	Zea mays response regulator 1. ZmRR1. cytokinin-inducible.

BAB17300.1 AB042260 Zea mays  
response regulator. ZmRR3.

BAB20582.1 AB042269 Zea mays  
response regulator 7. ZmRR7.

BAB41137.1 AB060130 Zea mays  
response regulator 8. ZmRR8.

SEQ ID NO: 925

AAA33280.1 L20475 Datura stramonium  
29kDa protein; high homology to aa sequence of tropinone reductases.

AAA33281.1 L20473 Datura stramonium  
catalyses a stereospecific reduction of tropinone to tropine. tropinone reductase-I.

BAA85844.1 AB026544 Hyoscyamus niger  
tropinone reductase-I. tr1.

CAC34420.1 AJ307584 Solanum tuberosum  
tropine forming tropinone reductase. tropinone reductase I. TRI.

BAA13547.1 D88156 Hyoscyamus niger  
tropinone reductase-I.

AAA33282.1 L20474 Datura stramonium  
catalyses a stereospecific reduction of tropinone to pseudotropine. tropinone reductase-II.

BAA85845.1 AB026545 Hyoscyamus niger  
tropinone reductase-II. tr2.

AAB09776.1 L20485 Hyoscyamus niger  
tropinone reductase-II.

CAB52307.1 AJ245634 Solanum tuberosum  
pseudotropine forming tropinone reductase. tropinone reductase II. TRII.

CAC19810.1 AJ292343 Solanum tuberosum  
pseudotropine forming tropinone reductase. tropinone reductase II. trII.

CAA45866.1 X64566 Cuphea lanceolata  
beta-ketoacyl-ACP reductase. Clkr27. 3-oxoacyl-[acyl-carrier protein] reductase.

CAA45793.1 X64463 Brassica napus  
3-oxoacyl-[acyl-carrier protein] reductase.

AAB82767.1 U89509 Zea mays  
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAB82766.1 U89510 Hordeum vulgare  
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAB20114.2 S60064 Brassica napus  
enoyl-acyl carrier protein reductase. This sequence comes from fig3; conceptual translation  
differs from published sequence.

CAA74176.1 Y13861 Nicotiana tabacum  
enoyl-ACP reductase. enr-T2.

AAB82764.1 U89511 Allium porrum  
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAC78100.1	AF093628	Oryza sativa protochlorophyllide reductase homolog.	
CAA74177.1	Y13862	Nicotiana tabacum enoyl-ACP reductase. enr-T1.	
			SEQ ID NO: 927
AAD43046.1	AF124045	Sorghum bicolor GTP-binding protein-like. 110K5.8. terminal exon, defined by homology to maize ESTs.	
			SEQ ID NO: 928
CAA09619.1	AJ011418	Lycopersicon esculentum ubiquitin activating enzyme.	
AAC32140.1	AF051239	Picea mariana probable ubiquitin activating enzyme 2. Sb53. similar to Arabidopsis thaliana ubiquitin activating enzyme 2 encoded by GenBank Accession Number U40566.	
AAA34308.1	M55604	Triticum aestivum ubiquitin-activating enzyme E1. UBA1.	
AAA34265.1	M90663	Triticum aestivum ubiquitin activating enyme. E1.	
AAA34266.1	M90664	Triticum aestivum ubiquitin activating enzyme. E1.	
CAA71762.1	Y10804	Nicotiana tabacum Ubiquitin activating enzyme E1. UBA1.	
			SEQ ID NO: 929
CAA55693.1	X79086	Zea mays initiator-binding protein. IBP2.	
CAC19789.1	AJ251686	Catharanthus roseus putative transcription factor. MYB-like DNA-binding protein. bpf-1.	
CAA55691.1	X79085	Zea mays initiator binding protein. IBP1.	
AAF97508.1	AF242298	Oryza sativa telomere binding protein-1. TBP1.	
			SEQ ID NO: 930
AAK15447.1	AC037426	Oryza sativa putative flavin-containing monooxygenase. OSJNBb0014I11.12.	
AAK15439.1	AC037426	Oryza sativa putative flavin-containing monooxygenase. OSJNBb0014I11.8.	
BAA88198.1	AP000837	Oryza sativa Similar to human dimethylaniline monooxygenase (AC002376).	
BAA88195.1	AP000837	Oryza sativa Similar to human dimethylaniline monooxygenase (AC002376).	
BAB32703.1	AP002902	Oryza sativa dimethylaniline monooxygenase-like protein. P0492F05.5. contains EST C72123(E1029).	

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BAB07916.2 AP002835 *Oryza sativa*  
dimethylaniline monooxygenase-like protein. P0417G05.24. contains EST C72123(E1029).

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SEQ ID NO: 931

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AAG38521.1 AF283536 *Citrus x paradisi*  
cystatin-like protein. cystein proteinase inhibitor.

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AAA97905.1 U51853 *Glycine max*  
cysteine proteinase inhibitor.

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CAA79954.1 Z21954 *Vigna unguiculata*  
cysteine proteinase inhibitor.

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AAB66355.1 U54702 *Oryza sativa*  
thiol proteinase inhibitor; cysteine proteinase inhibitor. oryzacystatin. has potential for insect resistance in rice and for cancer therapeutics.

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AAB24010.1 S49967 *Oryza*  
oryzacystatin. oryzacystatin. cysteine protease inhibitor; This sequence comes from Fig. 1.

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CAA60610.1 X87126 *Zea mays*  
cysteine proteinase inhibitor. zmc-II.

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BAA09666.1 D63342 *Zea mays*  
cysteine proteinase inhibitor. gCC.

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AAA32672.1 L16624 *Ambrosia artemisiifolia*  
cystatin proteinase inhibitor.

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BAA07327.1 D38130 *Zea mays*  
inhibition against cysteine proteinases. cystatin II.

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AAA97907.1 U51855 *Glycine max*  
cysteine proteinase inhibitor.

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BAB18766.1 AB038392 *Triticum aestivum*  
cysteine proteinase inhibitor. WC61. cystatin.

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BAB18767.1 AB038393 *Triticum aestivum*  
cysteine proteinase inhibitor. WC92. cystatin.

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CAA11899.1 AJ224331 *Castanea sativa*  
cysteine proteinase inhibitor. cystatin.

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AAB71505.1 U82220 *Pyrus communis*  
cysteine protease inhibitor.

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AAA79239.1 L48182 *Brassica rapa*  
cysteine proteinase inhibitor. N-terminal deletion clone; putative.

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CAA60634.1 X87168 *Sorghum bicolor*  
cysteine proteinase inhibitor. CPI1.

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AAA68150.1 L42819 *Brassica rapa*  
cysteine proteinase inhibitor. N-terminal deletion clone; putative.

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BAB18765.1 AB038391 *Triticum aestivum*  
cysteine proteinase inhibitor. gWC2. cystatin.

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BAB18768.1 AB038394 *Triticum aestivum*  
cysteine proteinase inhibitor. WC83. cystatin.

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AAC37479.1	L41355	Brassica rapa cysteine proteinase inhibitor.
BAA28867.1	AB014760	Cucumis sativus root-specific cysteine proteinase inhibitor. cysteine proteinase inhibitor.
AAD33907.1	AF143677	Artemisia vulgaris cysteine proteinase inhibitor. CPI. pollen cystatin.
BAA89582.1	AP001073	Oryza sativa ESTs AU067919(C10906),AU067918(C10906) correspond to a region of the predicted gene. Similar to cysteine proteinase inhibitor (D31700).
CAA72790.1	Y12068	Hordeum vulgare cysteine proteinase inhibitor. CPI.
AAA96316.1	U51119	Brassica rapa cysteine proteinase inhibitor. BCPI-2.
AAK15090.1	AF240007	Sesamum indicum cystatin. cysteine proteinase inhibitor.
AAF23127.1	AF198389	Lycopersicon esculentum cysteine proteinase inhibitor. cystatin. STC. expression induced by arachidonic acid and gamma linolenic acid.
BAA19610.1	D64115	Glycine max cysteine proteinase inhibitor. cystatin.
BAA19608.1	D31700	Glycine max cysteine proteinase inhibitor. cystatin.
CAA89697.1	Z49697	Ricinus communis cysteine proteinase inhibitor.
AAF72202.1	AF265551	Manihot esculenta cysteine protease inhibitor.
AAA97906.1	U51854	Glycine max cysteine proteinase inhibitor.
CAA50437.1	X71124	Carica papaya cysteine proteinase inhibitor (cystatin).
AAF23126.1	AF198388	Lycopersicon esculentum cysteine proteinase inhibitor. cystatin. LTC. expression induced by arachidonic acid and gamma linolenic acid.
AAD13812.1	AF117334	Ipomoea batatas cysteine proteinase inhibitor. cystatin.
AAF64480.1	AF241536	Ipomoea batatas cysteine protease inhibitor. CYSPI.
AAK30004.1	AY028994	Dianthus caryophyllus cysteine proteinase inhibitor. DC-CPIn.
BAB18769.1	AB038395	Triticum aestivum cysteine proteinase inhibitor. WC81. cystatin.
AAC32853.1	AF083253	Lycopersicon esculentum cysteine protease inhibitor.

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 SEQ ID NO: 938
 

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 CAA06486.1 AJ005340 *Linum usitatissimum*  
 IAA amidohydrolase. homolog.
 

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 SEQ ID NO: 940
 

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 BAB17350.1 AP002747 *Oryza sativa*  
 putative nodulin. P0698G03.34. contains ESTs  
 D39891(S1543),D41717(S4395),AU033037(S1543).
 

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 BAA85440.1 AP000616 *Oryza sativa*  
 ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.;  
 similar to *Medicago nodulin N21*-like protein (AC004218).
 

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 CAB53493.1 AJ245900 *Oryza sativa*  
 CAA303720.1 protein. q3037.20. Similar to *Medicago nodulin N21* (MtN21).
 

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 SEQ ID NO: 941
 

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 BAA21921.1 AB006599 *Petunia x hybrida*  
 ZPT2-12. C2H2 zinc finger protein, 2 finger.
 

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 BAA21922.1 AB006600 *Petunia x hybrida*  
 ZPT2-13. C2H2 zinc finger protein, 2finger.
 

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 BAA19110.1 AB000451 *Petunia x hybrida*  
 PEThy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.
 

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 BAA21923.1 AB006601 *Petunia x hybrida*  
 ZPT2-14. C2H2 zinc finger protein, 2 finger.
 

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 BAA21925.1 AB006603 *Petunia x hybrida*  
 ZPT2-8. C2H2 zinc finger protein, 2 finger.
 

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 BAA21924.1 AB006602 *Petunia x hybrida*  
 ZPT2-7. C2H2 zinc finger protein, 2finger.
 

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 BAA21920.1 AB006598 *Petunia x hybrida*  
 ZPT2-11. C2H2 zinc finger protein, 2finger.
 

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 CAA60828.1 X87374 *Pisum sativum*  
 putative zinc finger protein.
 

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 BAA19111.1 AB000452 *Petunia x hybrida*  
 PEThy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.
 

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 BAA21926.1 AB006604 *Petunia x hybrida*  
 ZPT2-9. C2H2 zinc finger protein, 2 finger.
 

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 BAA21927.1 AB006605 *Petunia x hybrida*  
 ZPT3-3. C2H2 zinc finger protein, 3 finger.
 

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 BAA96071.1 AB035133 *Petunia x hybrida*  
 C2H2 zinc-finger protein ZPT3-3. ZPT3-3.
 

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 BAA21919.1 AB006597 *Petunia x hybrida*  
 ZPT2-10. C2H2 zinc finger protein, 2 finger.
 

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 BAA96070.1 AB035132 *Petunia x hybrida*  
 C2H2 zinc-finger protein ZPT2-10. PEThy;ZPT2-10.
 

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 CAB77055.1 Y18788 *Medicago sativa*  
 putative TFIIIA (or kruppel)-like zinc finger protein.
 

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AAB53260.1	U76554	Brassica rapa transcription factor. zinc-finger protein-1. BR42.
AAB53261.1	U76555	Brassica rapa zinc-finger protein BcZFP1. BcZFP1(3-2z).
BAA19114.1	AB000455	Petunia x hybrida PEThy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
BAA05078.1	D26085	Petunia x hybrida zinc-finger DNA binding protein.
AAD26942.1	AF119050	Datisca glomerata zinc-finger protein 1. zfp1. DgZFP1.
BAA05077.1	D26084	Petunia x hybrida zinc-finger DNA binding protein.
AAB39638.1	U68763	Glycine max putative transcription factor. SCOF-1. scof-1. zinc-finger protein.
AAC06243.1	AF053077	Nicotiana tabacum transcription factor. osmotic stress-induced zinc-finger protein. zfp.
BAA19112.1	AB000453	Petunia x hybrida PEThy;ZPT3-1. Cys(2) zinc finger protein, 3 fingers.
AAK01713.1	AF332876	Oryza sativa zinc finger transcription factor ZF1.
BAA05076.1	D26083	Petunia x hybrida zinc-finger DNA binding protein.
BAA05079.1	D26086	Petunia x hybrida zinc-finger protein.
BAA21928.1	AB006606	Petunia x hybrida ZPT4-4. C2H2 zinc finger protein, 4 finger.
BAA19926.1	AB000456	Petunia x hybrida PEThy; ZPT4-2. C2H2 zinc finger protein, 4 finger.
BAA19113.1	AB000454	Petunia x hybrida PEThy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.
SEQ ID NO: 945		
AAG10793.1	AF296158	Citrus unshiu beta-carotene hydroxylase. CHX1.
AAG33636.1	AF315289	Citrus unshiu beta-carotene hydroxylase. CHX2. similar to beta-carotene hydroxylase of Citrus unshiu encoded by GenBank Accession Number AF296158.
AAG10430.1	AF251018	Tagetes erecta beta hydroxylase.
CAB55625.1	Y14809	Lycopersicon esculentum beta-carotene hydroxylase. CrtR-b1.
CAA70888.1	Y09722	Capsicum annuum beta-carotene hydroxylase 2.

CAB55626.1 Y14810 *Lycopersicon esculentum*  
beta-carotene hydroxylase. CrtR-b2.

CAA70427.1 Y09225 *Capsicum annuum*  
beta-carotene hydrolase.

CAC06712.1 AJ278882 *Narcissus pseudonarcissus*  
synthesis of zeaxanthin. beta-carotene hydroxylase.

AAD54243.1 AF162276 *Haematococcus pluvialis*  
carotenoid hydroxylase.

SEQ ID NO: 946

AAC18914.1 U94748 *Petunia x hybrida*

AN11. An11. No functional information available. Protein is involved in transcriptional regulation of anthocyanin biosynthesis in petunia. Protein contains five WD 40 repeats; WD 40 repeat protein.

SEQ ID NO: 948

AAG52887.1 AF333386 *Nicotiana tabacum*  
beta-expansin-like protein. PPAL. pollen allergen-like protein.

AAF72986.1 AF261273 *Oryza sativa*  
putative cell wall loosening activity. beta-expansin. EXPB5.

AAF72990.1 AF261277 *Oryza sativa*  
putative cell wall loosening activity. beta-expansin. EXPB9. putative group-1 pollen allergen.

BAB20817.1 AB051899 *Atriplex lentiformis*  
beta-expansin. A1-EXP1.

AAF72984.1 AF261271 *Oryza sativa*  
putative cell wall loosening activity. beta-expansin. EXPB3.

AAK15453.1 AC037426 *Oryza sativa*  
beta-expansin EXPB3. OSJNBb0014I11.1.

AAF72991.1 AF261278 *Oryza sativa*  
putative cell wall loosening activity. beta-expansin. EXPB10. putative group-1 pollen allergen.

AAK15442.1 AC037426 *Oryza sativa*  
beta-expansin EXPB6. OSJNBb0014I11.3.

AAF72987.1 AF261274 *Oryza sativa*  
putative cell wall loosening activity. beta-expansin. EXPB6.

AAF72983.1 AF261270 *Oryza sativa*  
putative cell wall loosening activity. beta-expansin. EXPB1. putative group-1 pollen allergen Ory s1.

AAF72988.1 AF261275 *Oryza sativa*  
putative cell wall loosening activity. beta-expansin. EXPB7.

AAF72989.2 AF261276 *Oryza sativa*  
putative cell wall loosening activity. beta-expansin. EXPB8.

AAF72985.1 AF261272 *Oryza sativa*  
putative cell wall loosening activity. beta-expansin. EXPB4.

AAK15440.1	AC037426	Oryza sativa beta-expansin EXPB2. OSJNBb0014I11.2.
AAB61710.1	U95968	Oryza sativa beta-expansin. EXPB2. cell wall loosening protein.
AAB37749.1	U30460	Cucumis sativus expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAD38296.1	AC007789	Oryza sativa putative expansin. OSJNBa0049B20.23.
BAB18336.1	AP002865	Oryza sativa putative expansin. P0034C11.27.
CAC19183.1	AJ291816	Cicer arietinum expansin.
AAG13983.1	AF297522	Prunus avium expansin 2. Exp2. PruavExp2.
AAG01875.1	AF291659	Striga asiatica alpha-expansin 3. Exp3.
AAG32920.1	AF184232	Lycopersicon esculentum expansin. Exp8.
AAC96077.1	AF049350	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAC96078.1	AF049351	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAF35902.1	AF230333	Zinnia elegans expansin 3.
BAA88200.1	AP000837	Oryza sativa EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAC39512.1	AF043284	Gossypium hirsutum expansin. GhEX1. contains N-terminal signal peptide.
AAD38297.1	AC007789	Oryza sativa putative expansin. OSJNBa0049B20.24.
AAF32411.1	AF230278	Triphysaria versicolor alpha-expansin 1.
BAB18338.1	AP002865	Oryza sativa putative expansin. P0034C11.29.
AAG32921.1	AF184233	Lycopersicon esculentum expansin. Exp10.
CAC19184.1	AJ291817	Cicer arietinum expansin.
AAC96079.1	AF049352	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.

SEQ ID NO: 950

CAA52213.1	X74115	Picea abies short-chain alcohol dehydrogenase.
AAC35342.1	AF072449	Ipomoea trifida short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAC35340.1	AF072447	Ipomoea trifida short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
CAA11153.1	AJ223177	Nicotiana tabacum short chain alcohol dehydrogenase.
CAA11154.1	AJ223178	Nicotiana tabacum short chain alcohol dehydrogenase. SCANT.
AAK29646.1	AF349916	Solanum tuberosum putative short-chain type alcohol dehydrogenase. GAN; similar to tomato Leert10 and maize Ts2.
AAC37345.1	L20621	Zea mays alcohol dehydrogenase. short chain.
AAC35341.1	AF072448	Ipomoea trifida short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAC35343.1	AF072450	Ipomoea trifida short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAB57737.1	U89270	Tripsacum dactyloides short-chain alcohol dehydrogenase. gynomonoecious sex form 1. similar to Zea mays tasselseed 2: SwissProt Accession Number P50160.
AAF89645.1	AF169018	Glycine max seed maturation protein PM34. PM34. similar to bacterial glucose and ribitol dehydrogenase.
AAF04253.1	AF097651	Pisum sativum short-chain alcohol dehydrogenase SAD-C. sadC. contains the entire nucleotide binding motif of 3(alpha), 20(beta)-hydroxysteroid dehydrogenases, GXXXXXXGXXG(A)XGXXXA (Ghosh et al., 1991, Proc. Natl. Acad. Sci. USA 88, 10064-10068).
AAF04193.1	AF053638	Pisum sativum short-chain alcohol dehydrogenase. sadA. contains the entire nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068); similar to Lycopersicon esculentum product encoded by GenBank Accession Number U21801 and Streptomyces hydrogenans steroid alcohol dehydrogenase.
AAB57738.1	U89271	Tripsacum dactyloides short-chain alcohol dehydrogenase. gynomonoecious sex form 1. similar to Zea mays tasselseed 2: SwissProt Accession Number P50160.
CAB91875.1	AJ277945	Lycopersicon esculentum putative alcohol dehydrogenase. yfe37.
AAF04194.1	AF053639	Pisum sativum short-chain alcohol dehydrogenase. sadB. contains the Prosite pattern no. PS00061 for short- chain alcohol dehydrogenases; contains a deletion in the nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068).

AAB00109.1	U21801	<i>Lycopersicon esculentum</i> alcohol dehydrogenase homolog. GAD3. mRNA is suppressed in the presence of gibberellin; similar to nonmetallo-short-chain alcohol dehydrogenases, PIR Accession Number A47542.
		SEQ ID NO: 952
CAB63264.1	AJ251808	<i>Lotus japonicus</i> calcium-binding protein. cbp1.
AAG43547.1	AF211529	<i>Nicotiana tabacum</i> Avr9/Cf-9 rapidly elicited protein 31. ACRE31. similar to <i>Solanum tuberosum</i> CAST calcium binding protein encoded by GenBank Accession Number L02830.
AAA34014.1	L01432	<i>Glycine max</i> calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA34013.1	L01430	<i>Glycine max</i> calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
AAA92681.1	U13882	<i>Pisum sativum</i> calcium-binding protein. calmodulin.
CAA78301.1	Z12839	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin. putative.
AAA19571.1	U10150	<i>Brassica napus</i> calcium binding. calmodulin. bcm1.
AAA85157.1	U20297	<i>Solanum tuberosum</i> calcium-binding protein. calmodulin.
AAA85156.1	U20296	<i>Solanum tuberosum</i> calcium-binding protein. calmodulin.
AAA62351.1	U20295	<i>Solanum tuberosum</i> calcium-binding protein. calmodulin.
AAA85155.1	U20294	<i>Solanum tuberosum</i> calcium-binding protein. calmodulin.
AAC49587.1	U49105	<i>Triticum aestivum</i> calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	<i>Triticum aestivum</i> calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	<i>Triticum aestivum</i> calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	<i>Triticum aestivum</i> calmodulin TaCaM3-1. calcium-binding protein.
AAC49580.1	U48689	<i>Triticum aestivum</i> calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	<i>Triticum aestivum</i> calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	<i>Triticum aestivum</i> calmodulin TaCaM1-1. calcium-binding.

---

CAA78287.1 Z12827 Oryza sativa  
calcium binding protein, signal transduction. calmodulin.

---

AAA03580.1 L01431 Glycine max  
calcium-binding regulatory protein. calmodulin. SCaM-2. putative.

---

AAA33901.1 L18913 Oryza sativa  
calcium binding protein, signal transduction. calmodulin. putative.

---

AAA34015.1 L01433 Glycine max  
calcium-binding regulatory protein. calmodulin. SCaM-4. putative.

---

**Table 24** Plant Open Reading Frames (ORFs) orthologous to specific *Chenopodium* ORFs

SEQ ID NO:1956	
CAB51903.1	AJ242807 <i>Brassica napus</i> endo-1,4-beta-D-glucanase. Cell16. cellulase.
BAA94257.1	AB040769 <i>Hordeum vulgare</i> endo-1,4-beta-glucanase Cell1. Cell1.
AAC49704.1	U78526 <i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase. Cel3.
SEQ ID NO:1957	
BAB21273.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.4.
BAB21275.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.6.
BAB21276.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
CAA94437.1	Z70524 <i>Spirodela polyrrhiza</i> multidrug resistance protein. PDR5-like ABC transporter.
BAB21279.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463),AU101680(R3463).
CAA03960.1	AJ000234 <i>Hordeum vulgare</i> partial sequence, homology to PDR5-like ABC transporter.
SEQ ID NO:1960	
AAD51778.1	AF116858 <i>Phaseolus vulgaris</i> utilizes UDPX as the sugar donor and catalyzes the formation of O-xylosylzeatin from zeatin. zeatin O-xylosyltransferase. ZOX1.
AAD04166.1	AF101972 <i>Phaseolus lunatus</i> catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
BAA36410.1	AB012114 <i>Vigna mungo</i> UDP-glycose:flavonoid glycosyltransferase. UFGlyT.
BAB17061.1	AP002523 <i>Oryza sativa</i> putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).

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BAA36412.1 AB012116 *Vigna mungo*  
UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

---

AAK28303.1 AF346431 *Nicotiana tabacum*  
phenylpropanoid:glucosyltransferase 1. togt1.  
glucosyltransferase.

---

BAB17059.1 AP002523 *Oryza sativa*  
putative glucosyl transferase. P0013F10.5.

---

AAF17551.1 AF198453 *Glycine max*  
UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

---

AAB36653.1 U32644 *Nicotiana tabacum*  
immediate-early salicylate-induced glucosyltransferase.  
IS5a.

---

CAB88666.1 AJ400861 *Cicer arietinum*  
flavonoid glycosyltransferase. putative UDP-glycose.

---

AAB36652.1 U32643 *Nicotiana tabacum*  
immediate-early salicylate-induced glucosyltransferase.  
IS10a.

---

CAA54612.1 X77462 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT5.

---

BAB17060.1 AP002523 *Oryza sativa*  
putative glucosyl transferase. P0013F10.6.

---

AAK28304.1 AF346432 *Nicotiana tabacum*  
phenylpropanoid:glucosyltransferase 2. togt2.  
glucosyltransferase.

---

CAA59450.1 X85138 *Lycopersicon esculentum*  
twi1. homologous to glucosyltransferases.

---

BAA83484.1 AB031274 *Scutellaria baicalensis*  
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

---

CAA54611.1 X77461 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT2.

---

BAA36411.1 AB012115 *Vigna mungo*  
UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

---

CAC35167.1 AJ310148 *Rauvolfia serpentina*  
arbutin synthase. as.

---

BAB17182.1 AP002843 *Oryza sativa*  
putative UTP-glucose glucosyltransferase. P0407B12.19.

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CAB56231.1 Y18871 *Dorotheanthus bellidiformis*  
betanidin-5-O-glucosyltransferase.

BAB17176.1 AP002843 *Oryza sativa*  
putative UTP-glucose glucosyltransferase. P0407B12.13.

AAK16172.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.14.

CAA54613.1 X77463 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT6.

AAF61647.1 AF190634 *Nicotiana tabacum*  
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA93039.1 AB033758 *Citrus unshiu*  
limonoid UDP-glucosyltransferase. LGTase.

CAA54610.1 X77460 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT4.

AAA59054.1 L34847 *Zea mays*  
conjugation of the growth hormone indole-3-acetic acid  
(IAA). IAA-glu synthetase. iaglu.

BAA36423.1 AB013598 *Verbena x hybrida*  
UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

AAF17077.1 AF199453 *Sorghum bicolor*  
UDP-glucose glucosyltransferase.  
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.

CAA54558.1 X77369 *Solanum melongena*  
glycosyl transferase. GT.

AAK16175.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.15.

CAA81057.1 Z25802 *Petunia x hybrida*  
UDP rhamnose: anthocyanidin-3-glucoside  
rhamnosyltransferase.

CAA50377.1 X71060 *Petunia x hybrida*  
anthocyanin: rhamnosyltransferase. rt.

CAA50376.1 X71059 *Petunia x hybrida*  
anthocyanin 3 glucoside: rhamnosyltransferase. rt.

AAK16181.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.16.

AAK16178.1 AC079887 *Oryza sativa*  
putative glucosyltransferase. OSJNBa0040E01.5.

AAD21086.1 AF127218 *Forsythia x intermedia*  
adds glucose residue to position 3 of flavonoid compounds.  
flavonoid 3-O-glucosyltransferase. UFGT.

BAA89008.1 AB027454 *Petunia x hybrida*  
anthocyanidin 3-O-glucosyltransferase. PGT8.

**SEQ ID NO:1962**

CAA65580.1 X96784 *Nicotiana tabacum*  
cytochrome P450. hsr515.

CAA64635.1 X95342 *Nicotiana tabacum*  
cytochrome P450. hsr515. hypersensitivity-related gene.

AAG44132.1 AF218296 *Pisum sativum*  
cytochrome P450. P450 isolog.

AAG49299.1 AF313489 *Callistephus chinensis*  
flavonoid 3',5'-hydroxylase.

BAA03438.1 D14588 *Petunia x hybrida*  
flavonoid-3',5'-hydroxylase. Hf1.

AAC32274.1 AF081575 *Petunia x hybrida*  
flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.

CAA50442.1 X71130 *Petunia x hybrida*  
P450 hydroxylase. PET 1.

CAA80266.1 Z22545 *Petunia x hybrida*  
flavonoid 3',5'-hydroxylase.

AAG49315.1 AF315465 *Pelargonium x hortorum*  
flavonoid 3'-hydroxylase.

AAG49298.1 AF313488 *Callistephus chinensis*  
putative flavonoid 3'-hydroxylase.

AAB17562.1 U72654 *Eustoma grandiflorum*  
flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

BAB20076.1 AB012925 *Torenia hybrida*  
flavonoid 3',5'-hydroxylase. F3'5'H.

AAG14961.1 AF214007 *Brassica napus*  
cytochrome p450-dependent monooxygenase. BNF5H1.

CAC26920.1 AJ295586 *Arabidopsis lyrata* subsp. *petraea*  
ferulate-5-hydroxylase. fah1.

AAG14962.1 AF214008 *Brassica napus*  
cytochrome p450-dependent monooxygenase. BNF5H2.

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15 All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied 20 considerably without departing from the basic principles of the invention.

**WHAT IS CLAIMED IS:**

1. A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen comprising:
  - 5 a) determining or detecting plant gene expression in an incompatible interaction; and
  - b) identifying at least one gene whose expression is significantly altered in the incompatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding compatible interaction.
- 10 2. A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen comprising:
  - a) determining or detecting plant gene expression in a compatible interaction; and
  - b) identifying at least one gene whose expression is significantly altered in the compatible
- 15 3. The method of claim 1 or 2 wherein the compatible interaction is between a plant having a resistance gene and a pathogen lacking a corresponding avirulence gene, a plant lacking a resistance gene to a pathogen having a corresponding avirulence gene, or a plant lacking a resistance gene and a pathogen lacking a corresponding avirulence gene.
- 20 4. The method of claim 1 or 2 wherein expression of the at least one gene is upregulated in response to infection.
- 25 5. The method of claim 1 or 2 wherein expression of the at least one gene is downregulated in response to infection.
- 30 6. The method of claim 1 or 2 wherein the at least one gene encodes a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOS: 1-953, 1954-1966, 2000-2129 or 2662-4737.

7. The method of claim 1 or 2 wherein the at least one gene comprises an open reading frame comprising one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.
8. The method of claim 1 or 2 wherein the pathogen is a bacterium.  
5
9. The method of claim 1 or 2 wherein the pathogen is a fungus.
10. The method of claim 1 or 2 wherein the pathogen is a virus.
11. The method of claim 1 or 2 wherein gene expression is detected or determined using a gene chip, a cDNA array, cDNA-AFLP, or differential display PCR  
10
12. The method of any one of claims 1 to 6 or 8 to 11 wherein the plant is a dicot.
13. The method of any one of claims 1 to 6 or 8 to 11 wherein the plant is a monocot.  
15
14. The method of any one of claims 1 to 13 further comprising isolating the at least one gene or a portion thereof which includes the open reading frame or promoter for the gene.
15. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that decreases jasmonic acid or ethylene-dependent signaling, comprising:
  - a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and  
20
  - b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having the mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.  
25  
30

16. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation in a gene that interferes with salicylic acid dependent signaling, comprising:

- a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.

15 17. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that results in enhanced susceptibility to bacterial infection, comprising:

- a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.

18. A method to identify at least one gene, the expression of which is altered by infection with 30 at least one virus, comprising:

- a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with a virus, so as to form a

complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and

5 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from an uninfected plant, so as to identify a gene, the expression of which is altered by virus infection.

19. A method to identify at least one gene, the expression of which is altered by infection with at least one pathogen comprising:

10 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from an incompatible interaction so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and

15 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from a corresponding compatible interaction so as to identify a gene, the expression of which is altered by the pathogen.

20 20. The method of any one of claims 15 to 19 wherein the at least one gene is upregulated.

21. The method of any one of claims 15 to 19 wherein the at least one gene is downregulated.

25 22. The method of any one of claims 15 to 19 wherein the gene which is identified encodes a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising any one of SEQ ID NOS:1-953, 1954-1966, 2000-2129 or 2662-4737.

23. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a dicot.

30 24. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a cereal plant.

25. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a monocot.
26. The method of any one of claims 15 to 19 further comprising identifying the promoter for 5 the at least one gene.
27. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide that is 10 substantially similar to a polypeptide encoded by a gene comprising a promoter selected from the group consisting of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
28. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, 15 which plant nucleotide sequence hybridizes under high stringency conditions to the complement of any one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
29. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant after pathogen infection, which 20 plant nucleotide sequence hybridizes under very high stringency conditions to the complement of any one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
30. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which plant 25 nucleotide sequence is selected from the group consisting of SEQ ID NOs:2137-2661 and or SEQ ID NOs:4738-6813.
31. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence is 25 to 2000 nucleotides in length.
32. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence has at least 90% nucleotide sequence identity to one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.

33. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence has at least 98% nucleotide sequence identity to one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.

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34. The polynucleotide of any one of claims 27 to 29 and 31 to 33 wherein the plant nucleotide sequence is from a dicot.

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35. The polynucleotide of any one of claims 26 to 29 and 31 to 33 wherein the plant nucleotide sequence is from a monocot.

36. The polynucleotide of any one of claims 26 to 29 and 31 to 33 wherein the plant nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.

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37. The polynucleotide of any one of claims 27 to 36 which comprises a TATA box, a CAAT box, or both.

20

38. A composition comprising the polynucleotide of any one of claims 27 to 37.

39. A recombinant vector comprising the polynucleotide of any one of claims 27 to 38.

40. The vector of claim 39 which is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor and phage.

25

41. An expression cassette comprising the polynucleotide of any one of claims 27 to 37 operatively linked to an open reading frame.

42. The expression cassette of claim 41 operably linked to other suitable regulatory sequences.

30

43. The expression cassette of claim 41 wherein the open reading frame is in an antisense orientation relative to the nucleotide sequence which alters transcription.

44. The expression cassette of claim 41 wherein the open reading frame is in a sense orientation relative to the nucleotide sequence which alters transcription.

45. A recombinant vector comprising the expression cassette of claim 41.

5

46. The vector of claim 45 wherein the vector is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor or phage.

47. A host cell comprising the expression cassette of claim 41.

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48. The host cell of claim 47 wherein the cell is selected from the group consisting of a yeast, a bacterium, a cereal plant cell, and an *Arabidopsis* cell.

49. A plant cell containing the expression cassette of claim 41.

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50. The plant cell of claim 49 which is a monocot cell.

51. The plant cell of claim 49 which is a dicot cell.

20 52. A transformed plant, the genome of which is augmented with the expression cassette of claim 41.

53. A transformed plant comprising transformed plant cells, which cells contain the expression cassette of claim 41.

25

54. The transformed plant of claim 52 or 53 which is a dicot.

55. The transformed plant of claim 52 or 53 which is a monocot.

30 56. The transformed plant of claim 52 or 53 which is selected from the group consisting of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.

57. A method for augmenting a plant genome, comprising:

- a) contacting plant cells with the expression cassette of claim 41 so as to yield a transformed plant cell; and
- b) regenerating the transformed plant cell to provide a differentiated transformed plant,  
5 wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.

58. A method to alter the phenotype of a plant cell comprising: introducing the expression cassette of claim 41 into a plant cell and expressing that open reading frame in the cell so  
10 as to alter a characteristic of that cell relative to a plant cell that does not comprise the expression cassette.

59. The method of claim 57 or 58 wherein the plant cell is a dicot cell.

15 60. The method of claim 57 or 58 wherein the plant is a monocot cell.

61. The method of claim 57 or 58 wherein the plant cell a cereal cell.

62. The method of claim 57 or 58 wherein the plant cell is selected from the group consisting  
20 of a cell of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut,  
sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.

63. The method of claim 57 or 58 wherein the open reading frame is in an antisense  
25 orientation relative to the nucleotide sequence which alters transcription.

64. The method of claim 57 or 58 wherein the expression inhibits transcription or translation  
of endogenous plant nucleic acid sequences corresponding to the open reading frame.

65. The method of claim 57 or 58 wherein the open reading frame is in a sense orientation  
30 relative to the nucleotide sequence which alters transcription.

66. The method of claim 57 wherein the open reading frame is expressed in an amount that is  
greater than the amount in a plant which does not comprise the expression cassette.

67. The method of claim 57 or 58 wherein the open reading frame encodes a protein.

68. The method of claim 67 wherein the protein encodes a regulatory product.

5

69. The method of claim 67 wherein the expression of the open reading frame confers insect resistance, bacterial resistance, fungal resistance, viral resistance, or nematode resistance.

70. A transformed plant prepared by the method of claim 57.

10

71. A product of the plant of claim 70 which comprises the expression cassette or the gene product encoded by the open reading frame.

72. The product of claim 71 which is selected from the group consisting of a seed, fruit, vegetable, transgenic plant, and a progeny plant.

15 73. A computer-readable medium having stored thereon a data structure comprising:

- a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a nucleotide molecule selected from the group consisting of SEQ ID NOs:1-953, 2137-2661, 1954-1966, 2000-2129, 2662-4737, 4738-6813 or the complement thereof; and
- b) a module receiving the nucleic acid molecule which compares the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

20 74. The computer readable medium of claim 73 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.

75. A computer-readable medium having stored thereon computer executable instructions for performing a method comprising:

30

- a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-953, 2137-2661, 1954-1966, 2000-2129, 2662-4737, 4738-6813 or the complement thereof; and

- b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

76. The computer readable medium of claim 75 wherein the medium is selected from the  
5 group consisting of magnetic tape, optical disk, CD-ROM, random access memory,  
volatile memory, non-volatile memory and bubble memory.

77. The computer readable medium of any one of claims 73 to 76 wherein the nucleotide  
sequence is not SEQ ID NOS. 1-208, 210-215, 217-261, 263-266, 268-316, 318-385, 387-  
10 424, 426-439, 441-799, or 801-953.

78. A method to confer resistance or tolerance to a plant to a pathogen, comprising:  
a) contacting plant cells with an expression cassette comprising a polynucleotide encoding  
15 a polypeptide that is substantially similar to a polypeptide encoded by an open reading  
frame comprising any one of SEQ ID NOS:1-953, 1954-1966, 2000-2129 or 2662-4737  
so as to yield transformed cells; and  
b) regenerating the transformed plant cells to provide a differentiated transformed plant,  
wherein the differentiated transformed plant expresses the polynucleotide in the cells of  
the plant in an amount effective to confer resistance or tolerance to the plant to a  
20 pathogen relative to a corresponding plant which does not comprise the expression  
cassette.

79. The method of claim 78 wherein the polynucleotide hybridizes under moderate stringency  
conditions to the complement of any one of SEQ ID NOS:1-953, 1954-1966, 2000-2129 or  
25 2662-4737.

80. The method of any one of claims 78 to 79 wherein the cells are monocot cells.

81. The method of any one of claims 78 to 79 wherein the cells are dicot cells.

30 82. The method of claim 78 wherein the open reading frame encodes a DNA binding protein,  
hormone response protein, membrane protein, metabolic protein, transposon,  
receptor/kinase, phosphatase, stress protein, cell wall protein, lipid transfer protein, heat

shock protein, protein processing protein, RNA processing protein, non-cell wall structural protein or a non-kinase signaling protein.

83. A transformed plant prepared by the method of any one of claims 78 to 82.

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84. A seed of the plant of claim 83.

85. A progeny plant of the plant of claim 83.

10 86. A method to identify a plant cell infected with a pathogen, comprising:

- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence corresponding to one of SEQ ID NOS:1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof, so as to yield an amplified product; and
- b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the amplified product is indicative of pathogen infection.

87. A method to identify a plant cell infected with a pathogen, comprising:

- a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOS:1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a complex, wherein the; and
- b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.

88. A method to identify a plant cell infected with a pathogen, comprising:

- a) contacting nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe corresponding to a sequence selected from the group consisting of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof, under stringent hybridization conditions to form a duplex, and

b) detecting or determining the presence or amount of the duplex, wherein the presence of a duplex is indicative of infection.

89. A method for marker-assisted breeding to select for plants having altered

5 resistance to a pathogen comprising:

a) contacting plant DNA or cDNA with a probe comprising a sequence selected from the group consisting of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof which hybridizes under moderate stringency conditions to a gene corresponding to one of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a duplex; and

10 b) detecting or determining the presence or amount of the duplex, wherein the amount or presence of the duplex is indicative of the presence of a gene, the expression of which alters the resistance of the plant to a pathogen.

15

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 01/01105

A. CLASSIFICATION OF SUBJECT MATTER  
 IPC 7 C12N15/29 C12N15/82 C12Q1/68 A01H5/00 G06F17/00  
 C07K14/415

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE, SEQUENCE SEARCH

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SCHENK P M ET AL: "Coordinated plant defense responses in <i>Arabidopsis</i> revealed by microarray analysis" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, US, vol. 97, no. 21, 10 October 2000 (2000-10-10), pages 11655-11660, XP002153163. ISSN: 0027-8424 the whole document ---	1-5, 8-21, 23-26
X	WO 97 49822 A (CIBA GEIGY AG ; ELLIS DANIEL MURRAY (US); FRIEDRICH LESLIE BETHARDS) 31 December 1997 (1997-12-31) the whole document ---	1-5, 8-21, 23-26 -/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

## \* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

9 July 2002

Date of mailing of the international search report

25.09.2002

Name and mailing address of the ISA

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 01/01105

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 07603 A (TUZUN SADIK ;UNIV AUBURN (US); ABDULLAH MALIKAH (US); SINGH NAREND) 1 February 2001 (2001-02-01) the whole document ---	1-5, 8-21, 23-26
X	EP 1 033 405 A (CERES INC) 6 September 2000 (2000-09-06)	73-76, 78-86, 88,89
A	page 1 -page 26 see SEQ IN NO: 38097 page 325 -page 341; claims 1-34 -----	6,7,22

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/IB 01/01105

### Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
  
2.  Claims Nos.: 87 because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210
  
3.  Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

### Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1.  As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3.  As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

Claims 1-26, 73-89 partially.

4.  No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

#### Remark on Protest

The additional search fees were accompanied by the applicant's protest.  
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 87

Present claim 87 relates to a product/compound defined by reference to a desirable characteristic or property, namely an agent that binds to a polypeptide encoded by an open reading frame.

The claims cover all products/compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such products/compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the product/compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, no search has been carried out.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-26, 73-89 partially

A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen wherein the gene encodes a polypeptide encoded by an open reading frame comprising SEQ ID NO: 1. A method to identify at least one gene, the expression of which is altered by pathogen infection, a computer-readable medium, a method to confer resistance or tolerance to a plant, a transformed plant, a seed, a method to identify a plant cell infected with a pathogen, a method for marker-assisted breeding comprising said nucleic acid.

Invention 2-3173: claims 1-26, 73-89 partially

same as invention 1 but comprising a gene in the order as given in claim 6 (invention 2 is limited to SEQ ID NO: 2 and invention 3173 is limited to SEQ ID NO: 4737).

Invention 3174: claims 26-77 partially

An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid comprising SEQ ID NO: 2137. A composition, a vector, an expression cassette, a host cell, a plant cell, a transformed plant, a method for augmenting a plant genome, a method to alter the phenotype of a plant cell, a computer-readable medium comprising said polynucleotide.

Invention 3174-5774: claims 26-77 partially

same as invention 3173 but comprising a promoter sequence in the order as given in claim 27 (invention 3174 comprises SEQ ID NO: 2138 and invention 5774 comprises SEQ ID NO: 6813).

**INTERNATIONAL SEARCH REPORT**

**Information on patent family members**

**International Application No**

**PCT/IB 01/01105**

Patent document cited in search report	Publication date	Patent family member(s)			Publication date
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		EP	1033405	A2	06-09-2000
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